

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

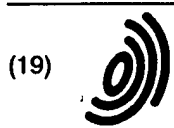
Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**



Europäisches Patentamt

European Patent Office

Office européen des brevets



(11) **EP 1 078 989 A2**

(12) **EUROPEAN PATENT APPLICATION**

(43) Date of publication:
28.02.2001 Bulletin 2001/09

(21) Application number: **00117807.8**

(22) Date of filing: **18.08.2000**

(51) Int. Cl.⁷: **C12N 15/53**, C12N 15/60,
C12N 1/21, C12N 1/20,
C12P 13/14, C12N 9/88,
C12N 9/06

(84) Designated Contracting States:
**AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU
MC NL PT SE**
Designated Extension States:
AL LT LV MK RO SI

(30) Priority: **20.08.1999 JP 23480699**
21.03.2000 JP 2000078771

(71) Applicant: **Ajinomoto Co., Ltd.**
Tokyo (JP)

(72) Inventors:
• **Izui, Hiroshi,**
c/o Ajinomoto Co., Inc.
Kawasaki-shi, Kanagawa (JP)
• **Moriya, Mika,**
c/o Ajinomoto Co., Inc.
Kawasaki-shi, Kanagawa (JP)

- **Hirano, Selko,**
c/o Ajinomoto Co., Inc.
Kawasaki-shi, Kanagawa (JP)
- **Hara, Yoshihiko,**
c/o Ajinomoto Co., Inc.
Kawasaki-shi, Kanagawa (JP)
- **Ito, Hisao,**
c/o Ajinomoto Co., Inc.
Kawasaki-shi, Kanagawa (JP)
- **Matsui, Kazuhiko,**
c/o Ajinomoto Co., Inc.
Kawasaki-shi, Kanagawa (JP)

(74) Representative:
Strehl Schübel-Hopf & Partner
Maximilianstrasse 54
80538 München (DE)

(54) **Method for producing L-glutamic acid by fermentation accompanied by precipitation**

(57) A microorganism which can metabolize a carbon source at a specific pH in a liquid medium containing L-glutamic acid at a saturation concentration and the carbon source, and has ability to accumulate L-glutamic acid in an amount exceeding the amount corresponding to the saturation concentration in the liquid medium at the pH; and a method for producing L-glutamic acid by fermentation, which comprises culturing the microorganism in a liquid medium of which pH is adjusted to a pH at which L-glutamic acid is precipitated, to produce and accumulate L-glutamic acid and precipitate L-glutamic acid in the medium.

EP 1 078 989 A2

Description

BACKGROUND OF THE INVENTION

5 [0001] The present invention relates to a method for producing L-glutamic acid by fermentation accompanied by precipitation. L-Glutamic acid is widely used as a material of seasonings and so forth.

[0002] L-Glutamic acid is mainly produced by fermentative methods using so-called coryneform bacteria producing L-glutamic acid and belonging to the genus *Brevibacterium*, *Corynebacterium* or *Microbacterium*, or mutant strains thereof (Amino Acid Fermentation, pp.195-215, Gakkai Shuppan Center, 1986). As methods for producing L-glutamic acid by fermentation by using other bacterial strains, there are known a method using a microorganism belonging to the genus *Bacillus*, *Streptomyces*, *Penicillium* or the like (U.S. Patent No. 3,220,929), a method using a microorganism belonging to the genus *Pseudomonas*, *Arthrobacter*, *Serratia*, *Candida* or the like (U.S. Patent No. 3,563,857), a method using a microorganism belonging to the genus *Bacillus*, *Pseudomonas*, *Serratia*, *Aerobacter aerogenes* (currently referred to as *Enterobacter aerogenes*) or the like (Japanese Patent Publication (Kokoku) No. 32-9393), a method using a mutant strain of *Escherichia coli* (Japanese Patent Application Laid-open (Kokai) No. 5-244970) and so forth. In addition, the inventors of the present invention have proposed a method for producing L-glutamic acid by using a microorganism belonging to the genus *Klebsiella*, *Erwinia* or *Pantoea* (Japanese Patent Application Laid-open No. 2000-106869).

[0003] Further, there have been disclosed various techniques for improving L-glutamic acid-producing ability by enhancing activities of L-glutamic acid biosynthetic enzymes through use of recombinant DNA techniques. For example, it has been reported that introduction of a gene coding for citrate synthase derived from *Escherichia coli* or *Corynebacterium glutamicum* was effective for enhancement of L-glutamic acid-producing ability in *Corynebacterium* or *Brevibacterium* bacteria (Japanese Patent Publication No. 7-121228). In addition, Japanese Patent Application Laid-open No. 61-268185 discloses a cell harboring recombinant DNA containing a glutamate dehydrogenase gene derived from *Corynebacterium* bacteria. Further, Japanese Patent Application Laid-open No. 63-214189 discloses a technique for improving L-glutamic acid-producing ability by amplifying a glutamate dehydrogenase gene, an isocitrate dehydrogenase gene, an aconitate hydratase gene and a citrate synthase gene.

[0004] Although L-glutamic acid productivity has been considerably increased by breeding of the aforementioned microorganisms or improvement of production methods, development of methods for more efficiently producing L-glutamic acid at a lower cost is required to respond to further increase of the demand in future.

[0005] There is known a method wherein fermentation is performed with crystallizing L-amino acid accumulated in culture (Japanese Patent Application Laid-open No. 62-288). In this method, the L-amino acid concentration in the culture is maintained below a certain level by precipitating the accumulated L-amino acid in the culture. Specifically, L-tryptophan, L-tyrosine or L-leucine is precipitated during fermentation by adjusting temperature and pH of the culture or adding a surface active agent to the medium.

[0006] While a fermentative method with precipitating L-amino acid is known as described above, amino acids suitable for this method are those of relatively low water solubility, and no example of applying the method to highly water-soluble amino acids such as L-glutamic acid is known. In addition, the medium must have low pH to precipitate L-glutamic acid. However, L-glutamic acid-producing bacteria such as those mentioned above cannot grow under acidic conditions, and therefore L-glutamic acid fermentation is performed under neutral conditions (U.S. Patent Nos. 3,220,929 and 3,032,474; Chao K.C. & Foster J.W., J. Bacteriol., 77, pp.715-725 (1959)). Thus, production of L-glutamic acid by fermentation accompanied by precipitation is not known. Furthermore, it is known that growth of most acidophile bacteria is inhibited by organic acids such as acetic acid, lactic acid and succinic acid (Yasuro Oshima Ed., "Extreme Environment Microorganism Handbook", p.231, Science Forum; Borichewski R.M., J. Bacteriol., 93, pp.597-599 (1967) etc.). Therefore, it is considered that many microorganisms are susceptible to L-glutamic acid, which is also an organic acid, under acidic conditions, and there has been no report that search of microorganisms showing L-glutamic acid-producing ability under acidic conditions was attempted.

SUMMARY OF THE INVENTION

50 [0007] In the aforementioned current situation, an object of the present invention is to search and breed a microorganism that produces L-glutamic acid under low pH conditions and to provide a method for producing L-glutamic acid using an obtained microorganism by fermentation with precipitating L-glutamic acid.

[0008] The inventors of the present invention considered during the study for improvement of L-glutamic acid productivity by fermentation that inhibition of the production by L-glutamic acid accumulated in a medium at a high concentration was one of obstructions to the improvement of productivity. For example, cells have an excretory system and an uptake system for L-glutamic acid. However, if L-glutamic acid once excreted into the medium is incorporated into cells again, not only the production efficiency falls, but also the L-glutamic acid biosynthetic reactions are inhibited as a

result. In order to avoid the inhibition of production by such accumulation of L-glutamic acid at high concentration, the inventors of the present invention screened microorganisms that can proliferate under acidic conditions and in the presence of a high concentration of L-glutamic acid. As a result, they successfully isolated microorganisms having such properties from a soil, and thus accomplished the present invention.

5 [0009] Thus, the present invention provides the followings.

(1) A microorganism which can metabolize a carbon source at a specific pH in a liquid medium containing L-glutamic acid at a saturation concentration and the carbon source, and has ability to accumulate L-glutamic acid in an amount exceeding the amount corresponding to the saturation concentration in the liquid medium at the pH.

10 (2) The microorganism according to (1), which can grow in the liquid medium.

(3) The microorganism according to (1) or (2), wherein the pH is not more than 5.0.

(4) The microorganism according to any one of (1) to (3), which has at least one of the following characteristics:

15 (a) the microorganism is enhanced in activity of an enzyme that catalyzes a reaction for biosynthesis of L-glutamic acid; and

(b) the microorganism is decreased in or deficient in activity of an enzyme that catalyzes a reaction branching from a biosynthetic pathway of L-glutamic acid and producing a compound other than L-glutamic acid.

20 (5) The microorganism according to (4), wherein the enzyme that catalyzes the reaction for biosynthesis of L-glutamic acid is at least one selected from citrate synthase, phosphoenolpyruvate carboxylase and glutamate dehydrogenase.

(6) The microorganism according to (4) or (5), wherein the enzyme that catalyzes the reaction branching from the biosynthetic pathway of L-glutamic acid and producing a compound other than L-glutamic acid is α -ketoglutarate dehydrogenase.

25 (7) The microorganism according to any one of (1) to (6), wherein the microorganism belongs to the genus *Enterobacter*.

(8) The microorganism according to (7), which is *Enterobacter agglomerans*.

(9) The microorganism according to (8), which has a mutation that causes less extracellular secretion of a viscous material compared with a wild strain when cultured in a medium containing a saccharide.

30 (10) A method for producing L-glutamic acid by fermentation, which comprises culturing a microorganism as defined in any one of (1) to (9) in a liquid medium of which pH is adjusted to a pH at which L-glutamic acid is precipitated, to produce and accumulate L-glutamic acid and precipitate L-glutamic acid in the medium.

35 (11) A method for screening a microorganism suitable for producing L-glutamic acid by fermentation with precipitating L-glutamic acid in a liquid medium, which comprises inoculating a sample containing microorganisms into an acidic medium containing L-glutamic acid at a saturation concentration and a carbon source, and selecting a strain that can metabolize the carbon source.

(12) The method according to (11), wherein a strain that can grow in the medium is selected as the strain that can metabolize the carbon source.

(13) The method according to (11) or (12), wherein a pH of the medium is not more than 5.0.

40

[0010] According to the method of the present invention, L-glutamic acid can be produced by fermentation with precipitating L-glutamic acid. As a result, L-glutamic acid in the medium is maintained below a certain concentration, and L-glutamic acid can be produced without suffering from the product inhibition by L-glutamic acid at a high concentration.

45 BRIEF EXPLANATION OF THE DRAWINGS

[0011]

Fig. 1 shows a restriction map of a DNA fragment derived from *Enterobacter agglomerans* pTWVEK101.

50 Fig. 2 shows comparison of the amino acid sequence deduced from the nucleotide sequence of the *sucA* gene derived from *Enterobacter agglomerans* and that derived from *Escherichia coli*. Upper sequence: *Enterobacter agglomerans*, lower sequence: *Escherichia coli* (the same shall apply hereafter).

Fig. 3 shows comparison of the amino acid sequence deduced from the nucleotide sequence of the *sucB* gene derived from *Enterobacter agglomerans* and that derived from *Escherichia coli*.

55 Fig. 4 shows comparison of the amino acid sequence deduced from the nucleotide sequence of the *sdhB* gene derived from *Enterobacter agglomerans* and that derived from *Escherichia coli*.

Fig. 5 shows comparison of the amino acid sequence deduced from the nucleotide sequence of the *sucC* gene derived from *Enterobacter agglomerans* and that derived from *Escherichia coli*.

Fig. 6 shows construction of plasmid pMWCPG having a *gltA* gene, a *ppc* gene and a *gdhA* gene.

Fig. 7 shows construction of plasmid RSF-Tet having the replication origin of the broad host spectrum plasmid RSF1010 and a tetracycline resistance gene.

Fig. 8 shows construction of plasmid RSFCPG having the replication origin of the broad host spectrum plasmid RSF1010, a tetracycline resistance gene, a *gltA* gene, a *ppc* gene and a *gdhA* gene.

Fig. 9 shows construction of plasmid pSTVCB having a *gltA* gene.

DETAILED DESCRIPTION OF THE INVENTION

Hereafter, the present invention will be explained in detail.

[0013] The microorganism of the present invention is a microorganism that (1) can metabolize a carbon source at a specific pH in a liquid medium containing L-glutamic acid at a saturation concentration and the carbon source and (2) has ability to accumulate L-glutamic acid in an amount exceeding the amount corresponding to the saturation concentration in the liquid medium at the pH.

[0014] The term "saturation concentration" means a concentration of L-glutamic acid dissolved in a liquid medium when the liquid medium is saturated with L-glutamic acid.

[0015] Hereafter, a method for screening a microorganism that can metabolize a carbon source in a liquid medium containing L-glutamic acid at a saturation concentration and the carbon source at a specific pH will be described. A sample containing microorganisms is inoculated into a liquid medium containing L-glutamic acid at a saturation concentration and a carbon source at a specific pH, and a strain that can metabolize the carbon source is selected. The specific pH is not particularly limited, but is usually not more than about 5.0, preferably not more than about 4.5, more preferably not more than about 4.3. The microorganism of the present invention is used to produce L-glutamic acid by fermentation with precipitating L-glutamic acid. If the pH is too high, it becomes difficult to allow the microorganism to produce L-glutamic acid enough for precipitation. Therefore, pH is preferably in the aforementioned range.

[0016] If pH of an aqueous solution containing L-glutamic acid is lowered, the solubility of L-glutamic acid significantly falls around pKa of γ -carboxyl group (4.25, 25°C). The solubility becomes the lowest at the isoelectric point (pH 3.2) and L-glutamic acid exceeding the amount corresponding to the saturation concentration is precipitated. While it depends on the medium composition, L-glutamic acid is usually dissolved in an amount of 10 to 20 g/L at pH 3.2, 30 to 40 g/L at pH 4.0 and 50 to 60 g/L at pH 4.7, at about 30°C. Usually pH does not need to be made below 3.0, because the L-glutamic acid precipitating effect plateaus when pH goes below a certain value. However, pH may be below 3.0.

[0017] In addition, the expression that a microorganism "can metabolize the carbon source" means that it can proliferate or can consume the carbon source even though it cannot proliferate, that is, it indicates that it catabolizes carbon sources such as saccharides or organic acids. Specifically, for example, if a microorganism proliferates when cultured in a liquid medium containing L-glutamic acid at a saturation concentration at pH 5.0 to 4.0, preferably pH 4.5 to 4.0, more preferably pH 4.3 to 4.0, still more preferably pH 4.0 at an appropriate temperature, for example, 28°C, 37°C or 50°C for 2 to 4 days, this microorganism can metabolize the carbon source in the medium. Further, for example, even if a microorganism does not proliferate when it is cultured in a liquid medium containing L-glutamic acid at a saturation concentration at pH 5.0 to 4.0, preferably pH 4.5 to 4.0, more preferably pH 4.3 to 4.0, still more preferably pH 4.0 at an appropriate temperature, for example, 28°C, 37°C or 50°C for 2 to 4 days, the microorganism which consumes the carbon source in the medium is that can metabolize the carbon source in the medium.

[0018] The microorganism which can metabolize the carbon source includes a microorganism which can grow in the liquid medium.

[0019] The expression that a microorganism "can grow" means that it can proliferate or can produce L-glutamic acid even though it cannot proliferate. Specifically, for example, if a microorganism proliferates when cultured in a liquid medium containing L-glutamic acid at a saturation concentration at pH 5.0 to 4.0, preferably pH 4.5 to 4.0, more preferably pH 4.3 to 4.0, still more preferably pH 4.0 at an appropriate temperature, for example, 28°C, 37°C or 50°C for 2 to 4 days, this microorganism can grow in the medium. Further, for example, even if a microorganism does not proliferate when it is cultured in a liquid synthetic medium containing L-glutamic acid at a saturation concentration at pH 5.0 to 4.0, preferably pH 4.5 to 4.0, more preferably pH 4.3 to 4.0, still more preferably pH 4.0 at an appropriate temperature, for example, 28°C, 37°C or 50°C for 2 to 4 days, the microorganism which increases the amount of L-glutamic acid in the medium is that can grow in the medium.

[0020] The selection described above may be repeated two or more times under the same conditions or with changing pH or the concentration of L-glutamic acid. An initial selection can be performed in a medium containing L-glutamic acid at a concentration lower than the saturation concentration, and thereafter a subsequent selection can be performed in a medium containing L-glutamic acid at a saturation concentration. Further, strains with favorable properties such as superior proliferation rate may be selected.

[0021] In addition to the property described above, the microorganism of the present invention has ability to accumulate L-glutamic acid in an amount exceeding the amount corresponding to the saturation concentration of L-glutamic

acid in a liquid medium. The pH of the aforementioned liquid medium is preferably the same as or close to that of the medium used for screening a microorganism having the aforementioned property (1). Usually, a microorganism becomes susceptible to L-glutamic acid at a high concentration as pH becomes lower. Therefore, it is preferred that pH is not low from the viewpoint of resistance to L-glutamic acid, but low pH is preferred from the viewpoint of production of L-glutamic acid with precipitating it. To satisfy these conditions, pH may be in the range of 3 to 5, preferably 4 to 5, or preferably 4.0 to 4.7, still more preferably 4.0 to 4.5, particularly preferably 4.0 to 4.3.

[0022] As the microorganism of the present invention or breeding materials therefor, there can be mentioned, for example, microorganisms belonging to the genus *Enterobacter*, *Klebsiella*, *Serratia*, *Pantoea*, *Erwinia*, *Escherichia*, *Corynebacterium*, *Alicyclobacillus*, *Bacillus*, *Saccharomyces* or the like. Among these, microorganisms belonging to the genus *Enterobacter* are preferred. Hereafter, the microorganism of the present invention will be explained mainly for microorganisms belonging to the genus *Enterobacter*, but the present invention can be applied to microorganism belonging to other genera and not limited to the genus *Enterobacter*.

[0023] As microorganisms belonging to the *Enterobacter*, there can be specifically mentioned *Enterobacter agglomerans*, preferably the *Enterobacter agglomerans* AJ13355 strain. This strain was isolated from a soil in Iwata-shi, Shizuoka, Japan as a strain that can proliferate in a medium containing L-glutamic acid and a carbon source at low pH.

[0024] The physiological properties of AJ13355 are as follows:

- (1) Gram staining: negative
- (2) Behavior against oxygen: facultative anaerobic
- (3) Catalase: positive
- (4) Oxidase: negative
- (5) Nitrate-reducing ability: negative
- (6) Voges-Proskauer test: positive
- (7) Methyl Red test: negative
- (8) Urease: negative
- (9) Indole production: positive
- (10) Motility: motile
- (11) H₂S production in TSI medium: weakly active
- (12) β -galactosidase: positive
- (13) Saccharide-assimilating property:

- Arabinose: positive
- Sucrose: positive
- Lactose: positive
- Xylose: positive
- Sorbitol: positive
- Inositol: positive
- Trehalose: positive
- Maltose: positive
- Glucose: positive
- Adonitol: negative
- Raffinose: positive
- Salicin: negative
- Melibiose: positive

- (14) Glycerol-assimilating property: positive
- (15) Organic acid-assimilating property:

- Citric acid: positive
- Tartaric acid: negative
- Gluconic acid: positive
- Acetic acid: positive
- Malonic acid: negative

- (16) Arginine hydrolase: negative
- (17) Ornithine decarboxylase: negative
- (18) Lysine decarboxylase: negative

(19) Phenylalanine deaminase: negative

(20) Pigment formation: yellow

(21) Gelatin liquefaction ability: positive

(22) Growth pH: growth is possible at pH 4.0, good growth at pH 4.5 to 7

(23) Growth temperature: good growth at 25°C, good growth at 30°C, good growth at 37°C, growth is possible at 42°C, growth is not possible at 45°C

[0025] Based on these bacteriological properties, AJ13355 was determined as *Enterobacter agglomerans*.

[0026] The *Enterobacter agglomerans* AJ13355 was deposited at the National Institute of Bioscience and Human-Technology, Agency of Industrial Science and Technology, Ministry of International Trade and Industry (postal code: 305-8566, 1-3, Higashi 1-chome, Tsukuba-shi, Ibaraki, Japan) on February 19, 1998 and received an accession number of FERM P-16644. It was then transferred to an international deposition under the provisions of Budapest Treaty on January 11, 1999 and received an accession number of FERM BP-6614.

[0027] The microorganism of the present invention may be a microorganism originally having L-glutamic acid-producing ability or one having L-glutamic acid-producing ability imparted or enhanced by breeding through use of mutation treatment, recombinant DNA techniques or the like.

[0028] L-Glutamic acid-producing ability can be imparted or enhanced by, for example, increasing activity of an enzyme that catalyzes a reaction for biosynthesis of L-glutamic acid. L-Glutamic acid-producing ability can also be enhanced by decreasing activity of an enzyme that catalyzes a reaction branching from the biosynthetic pathway of L-glutamic acid and producing a compound other than L-glutamic acid, or making the activity deficient.

[0029] As enzymes that catalyze a reaction for biosynthesis of L-glutamic acid, there can be mentioned glutamate dehydrogenase (hereafter, also referred to as "GDH"), glutamine synthetase, glutamate synthase, isocitrate dehydrogenase, aconitate hydratase, citrate synthase (hereafter, also referred to as "CS"), phosphoenolpyruvate carboxylase (hereafter, also referred to as "PEPC"), pyruvate dehydrogenase, pyruvate kinase, enolase, phosphoglyceromutase, phosphoglycerate kinase, glyceraldehyde-3-phosphate dehydrogenase, triosephosphate isomerase, fructose bisphosphate aldolase, phosphofructokinase, glucose phosphate isomerase and so forth. Among these enzymes, one, two or three of CS, PEPC and GDH are preferred. Further, it is preferred that the activities of all the three enzymes, CS, PEPC and GDH, are enhanced in the microorganism of the present invention. In particular, CS of *Brevibacterium lactofermentum* is preferred, because it does not suffer from inhibition by α -ketoglutaric acid, L-glutamic acid and NADH.

[0030] In order to enhance the activity of CS, PEPC or GDH, for example, a gene coding for CS, PEPC or GDH may be cloned on an appropriate plasmid and a host microorganism may be transformed with the obtained plasmid. The copy number of the gene coding for CS, PEPC or GDH (hereafter, abbreviated as "gltA gene", "ppc gene" and "gdhA gene", respectively) in the transformed strain cell increases, resulting in the increase of the activity of CS, PEPC or GDH.

[0031] The cloned gltA gene, ppc gene and gdhA gene are introduced into the aforementioned starting parent strain solely or in combination of arbitrary two or three kinds of them. When two or three kinds of the genes are introduced, two or three kinds of the genes may be cloned on one kind of plasmid and introduced into the host, or separately cloned on two or three kinds of plasmids that can coexist and introduced into the host.

[0032] Two or more kinds of genes coding for enzymes of the same kind, but derived from different microorganisms may be introduced into the same host.

[0033] The plasmids described above are not particularly limited so long as they are autonomously replicable in cells of a microorganism belonging to, for example, the genus *Enterobacter* or the like, but, for example, there can be mentioned pUC19, pUC18, pBR322, pHSG299, pHSG298, pHSG399, pH SG398, RSF1010, pMW119, pMW118, pMW219, pMW218, pACYC177, pACYC184 and so forth. Besides these, vectors of phage DNA can also be used.

[0034] Transformation can be performed by, for example, the method of D.M. Morrison (Methods in Enzymology, 68, 326 (1979)), the method wherein permeability of DNA is increased by treating recipient bacterium cells with calcium chloride (Mandel M. and Higa A., J. Mol. Biol., 53, 159 (1970)), the electroporation (Miller J.H., "A Short Course in Bacterial Genetics", Cold Spring Harbor Laboratory Press, U.S.A. 1992) or the like.

[0035] The activity of CS, PEPC or GDH can also be increased by allowing multiple copies of a gltA gene, a ppc gene or a gdhA gene to be present on chromosomal DNA of the aforementioned starting parent strain to be a host. In order to introduce multiple copies of the gltA gene, the ppc gene or the gdhA gene on chromosomal DNA of a microorganism belonging to the genus *Enterobacter* or the like, a sequence of which multiple copies are present on the chromosomal DNA, such as repetitive DNA and inverted repeats present at termini of a transposable element, can be used.

Alternatively, multiple copies of the genes can be introduced onto chromosomal DNA by utilizing transfer of a transposon containing the gltA gene, the ppc gene or the gdhA gene. As a result, the copy number of the gltA gene, the ppc gene or the gdhA gene in a transformed strain cell is increased, and thus the activity of CS, PEPC or GDH is increased.

[0036] As organisms to be a source of the gltA gene, the ppc gene or the gdhA gene of which copy number is

increased, any organism can be used so long as it has activity of CS, PEPC or GDH. In addition, bacteria, which are prokaryotes, for example, those belonging to the genus *Enterobacter*, *Klebsiella*, *Erwinia*, *Pantoea*, *Serratia*, *Escherichia*, *Corynebacterium*, *Brevibacterium* and *Bacillus* are preferred. As specific examples, there can be mentioned *Escherichia coli*, *Brevibacterium lactofermentum* and so forth. The *gltA* gene, the *ppc* gene and the *gdhA* gene can be obtained from chromosomal DNA of the microorganisms described above.

[0037] The *gltA* gene, the *ppc* gene and the *gdhA* gene can be obtained by using a mutant strain which is deficient in the activity of CS, PEPC or GDH to isolate a DNA fragment which complements the auxotrophy from chromosomal DNA of the aforementioned microorganisms. Since the nucleotide sequences of these genes of *Escherichia* and *Corynebacterium* bacteria have already been elucidated (Biochemistry, 22, pp.5243-5249 (1983); J. Biochem., 95, pp.909-916 (1984); Gene, 27, pp.193-199 (1984); Microbiology, 140, pp.1817-1828 (1994); Mol. Gen. Genet., 218, pp.330-339 (1989); Molecular Microbiology, 6, pp.317-326 (1992)), they can also be obtained by PCR utilizing primers synthesized based on each nucleotide sequence and chromosomal DNA as a template.

[0038] The activity of CS, PEPC or GDH can also be increased by enhancing the expression of the *gltA* gene, the *ppc* gene or the *gdhA* gene besides the aforementioned amplification of the genes. For example, the expression can be enhanced by replacing a promoter for the *gltA* gene, the *ppc* gene or the *gdhA* gene with other stronger promoters. For example, *lac* promoter, *trp* promoter, *trc* promoter, *tac* promoter, P_R promoter and P_L promoter of the lambda phage and so forth are known as strong promoters. The *gltA* gene, the *ppc* gene and the *gdhA* gene of which promoter is replaced are cloned on a plasmid and introduced into the host microorganism, or introduced onto the chromosomal DNA of the host microorganism by using repetitive DNA, inverted repeats, transposon or the like.

[0039] The activity of CS, PEPC or GDH can also be enhanced by replacing the promoter of the *gltA* gene, the *ppc* gene or the *gdhA* gene on the chromosome with other stronger promoters (see WO 87/03006 and Japanese Patent Application Laid-open No. 61-268183), or inserting a strong promoter in the upstream of the coding sequence of each gene (see Gene, 29, pp.231-241 (1984)). Specifically, homologous recombination can be performed between DNA containing the *gltA* gene, the *ppc* gene or the *gdhA* gene of which promoter is replaced with a stronger one or a part thereof and the corresponding gene on the chromosome.

[0040] Examples of the enzyme which catalyze a reaction branching from the biosynthetic pathway of the L-glutamic acid and producing a compound other than L-glutamic acid include α -ketoglutarate dehydrogenase (hereafter, also referred to as " α KGDH"), isocitrate lyase, phosphate acetyltransferase, acetate kinase, acetohydroxy acid synthase, acetolactate synthase, formate acetyltransferase, lactate dehydrogenase, glutamate decarboxylase, 1-pyrroline dehydrogenase and so forth. Among these enzymes, α KGDH is preferred.

[0041] In order to obtain decrease or deficiency of the activity of the aforementioned enzyme in a microorganism belonging to the genus *Enterobacter* or the like, mutation causing decrease or deficiency of the intracellular activity of the enzyme can be introduced into the gene of the aforementioned enzyme by a usual mutagenesis or genetic engineering method.

[0042] Examples of the mutagenesis method include, for example, methods utilizing irradiation with X-ray or ultraviolet ray, methods utilizing treatment with a mutagenic agent such as N-methyl-N'-nitro-N-nitrosoguanidine, and so forth. The site where the mutation is introduced to the gene may be in a coding region coding for an enzyme protein, or a region for regulating expression such as a promoter.

[0043] Examples of the genetic engineering methods include, for example, methods utilizing gene recombination, transduction, cell fusion and so forth. For example, a drug resistance gene is inserted into a cloned target gene to prepare a gene that has lost its function (defective gene). Subsequently, this defective gene is introduced into a cell of a host microorganism, and the target gene on the chromosome is replaced with the aforementioned defective gene by utilizing homologous recombination (gene disruption).

[0044] Decrease or deficiency of intracellular activity of the target enzyme and the degree of decrease of the activity can be determined by measuring the enzyme activity of a cell extract or a purified fraction thereof obtained from a candidate strain and comparing with that of a wild strain. For example, the α KGDH activity can be measured by the method of Reed et al. (Reed L.J. and Mukherjee B.B., Methods in Enzymology, 13, pp.55-61 (1969)).

[0045] Depending on the target enzyme, the target mutant strain can be selected based on the phenotype of the mutant strain. For example, a mutant strain which is deficient in the α KGDH activity or decreases in the α KGDH activity cannot proliferate or shows a markedly reduced proliferation rate in a minimal medium containing glucose or a minimal medium containing acetic acid or L-glutamic acid as an exclusive carbon source under aerobic conditions. However, normal proliferation is enabled even under the same condition by adding succinic acid or lysine, methionine and diaminopimelic acid to a minimal medium containing glucose. By utilizing these phenomena as indicators, mutant strains with decreased α KGDH activity or deficient in the activity can be selected.

[0046] A method for preparing the α KGDH gene deficient strain of *Brevibacterium lactofermentum* by utilizing homologous recombination is described in detail in WO 95/34672. Similar methods can be applied to the other microorganisms.

[0047] Further, techniques such as cloning of genes and cleavage and ligation of DNA, transformation and so forth

are described in detail in Molecular cloning, 2nd Edition, Cold Spring Harbor Press, 1989 and so forth.

[0048] As a specific example of a mutant strain deficient in α KGDH activity or with decreased α KGDH activity obtained as described above, there can be mentioned *Enterobacter agglomerans* AJ13356. *Enterobacter agglomerans* AJ13356 was deposited at the National Institute of Bioscience and Human-Technology, Agency of Industrial Science and Technology, Ministry of International Trade and Industry (postal code: 305-8566, 1-3, Higashi 1-chome, Tsukuba-shi, Ibaraki, Japan) on February 19, 1998 and received an accession number of FERM P-16645. It was then transferred to an international deposition under the provisions of Budapest Treaty on January 11, 1999 and received an accession number of FERM BP-6615. The *Enterobacter agglomerans* AJ13356 is deficient in α KGDH activity as a result of disruption of the α KGDH-E1 subunit gene (*sucA*).

[0049] When *Enterobacter agglomerans*, an example of the microorganism used in the present invention, is cultured in a medium containing a saccharide, a viscous material is extracellularly secreted, resulting in low operation efficiency. Therefore, when *Enterobacter agglomerans* having such a property of secreting the viscous material is used, it is preferable to use a mutant strain that secretes less the viscous material compared with a wild strain. Examples of mutagenesis methods include, for example, methods utilizing irradiation with X ray or ultraviolet ray, method utilizing treatment with a mutagenic agent such as N-methyl-N'-nitro-N-nitrosoguanidine and so forth. A mutant strain with decreased secretion of the viscous material can be selected by inoculating mutagenized bacterial cells in a medium containing a saccharide, for example, LB medium plate containing 5 g/L of glucose, culturing them with tilting the plate about 45 degrees and selecting a colony which does not show flowing down of liquid.

[0050] In the present invention, impartation or enhancement of L-glutamic acid-producing ability and impartation of other favorable properties such as mutation for less viscous material secretion described above can be carried out in an arbitrary order.

[0051] By culturing the microorganism of the present invention in a liquid medium of which pH is adjusted to a pH at which L-glutamic acid is precipitated, L-glutamic acid can be produced and accumulated with precipitating it in the medium. L-Glutamic acid can also be precipitated by starting the culture at a neutral pH and then ending it at a pH at which L-glutamic acid is precipitated.

[0052] The pH at which L-glutamic acid is precipitated means one at which L-glutamic acid is precipitated when the microorganism produces and accumulates L-glutamic acid.

[0053] As the aforementioned medium, a usual nutrient medium containing a carbon source, a nitrogen source, mineral salts and organic trace nutrients such as amino acids and vitamins as required can be used so long as pH is adjusted to a pH at which L-glutamic acid is precipitated. Either a synthetic medium or a natural medium can be used. The carbon source and the nitrogen source used in the medium can be any ones so long as they can be used by the cultured strain.

[0054] As the carbon source, saccharides such as glucose, glycerol, fructose, sucrose, maltose, mannose, galactose, starch hydrolysate and molasses are used. In addition, organic acids such as acetic acid and citric acid may be used each alone or in combination with another carbon source.

[0055] As the nitrogen source, ammonia, ammonium salts such as ammonium sulfate, ammonium carbonate, ammonium chloride, ammonium phosphate and ammonium acetate, nitrates and so forth are used.

[0056] As the organic trace nutrients, amino acids, vitamins, fatty acids, nucleic acids, those containing these substances such as peptone, casamino acid, yeast extract and soybean protein decomposition products are used. When an auxotrophic mutant strain that requires an amino acid and so forth for metabolization or growth is used, the required nutrient must be supplemented.

[0057] As mineral salts, phosphates, magnesium salts, calcium salts, iron salts, manganese salts and so forth are used.

[0058] As for the culture method, aeration culture is usually performed with controlling the fermentation temperature to be 20 to 42°C and pH to be 3 to 5, preferably 4 to 5, more preferably 4 to 4.7, particularly preferably 4 to 4.5. Thus, after about 10 hours to 4 days of culture, a substantial amount of L-glutamic acid is accumulated in the culture. Accumulated L-glutamic acid exceeding the amount corresponding to the saturation concentration is precipitated in the medium.

[0059] After completion of the culture, L-glutamic acid precipitated in the culture can be collected by centrifugation, filtration or the like. L-Glutamic acid dissolved in the medium can be collected according to known methods. For example, the L-glutamic acid can be isolated by concentrating the culture broth to crystallize it or isolated by ion exchange chromatography or the like. L-Glutamic acid precipitated in the culture broth may be isolated together with L-glutamic acid that have been dissolved in the medium after it is crystallized.

[0060] According to the method of the present invention, L-glutamic acid exceeding the amount corresponding to the saturation concentration is precipitated, and the concentration of L-glutamic acid dissolved in the medium is maintained at a constant level. Therefore, influence of L-glutamic acid at a high concentration on microorganisms can be reduced. Accordingly, it becomes possible to breed a microorganism having further improved L-glutamic acid-producing ability. Further, since L-glutamic acid is precipitated as crystals, acidification of the culture broth by accumulation of L-

glutamic acid is suppressed, and therefore the amount of alkali used for maintaining pH of the culture can significantly be reduced.

EXAMPLES

[0061] Hereafter, the present invention will be more specifically explained with reference to the following examples.

(1) Screening of microorganism having L-glutamic acid resistance in acidic environment

[0062] Screening of a microorganism having L-glutamic acid resistance in an acidic environment was performed as follows. Each of about 500 samples obtained from nature including soil, fruits, plant bodies, river water in an amount of 1 g was suspended in 5 mL of sterilized water, of which 200 μ L was coated on 20 mL of solid medium of which pH was adjusted to 4.0 with HCl. The composition of the medium was as follows: 3 g/L of glucose, 1 g/L of $(\text{NH}_4)_2\text{SO}_4$, 0.2 g/L of $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 0.5 g/L of KH_2PO_4 , 0.2 g/L of NaCl, 0.1 g/L of $\text{CaCl}_2 \cdot 7\text{H}_2\text{O}$, 0.01 g/L of $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$, 0.01 g/L of $\text{MnSO}_4 \cdot 4\text{H}_2\text{O}$, 0.72 mg/L of $\text{ZnSO}_4 \cdot 2\text{H}_2\text{O}$, 0.64 mg/L of $\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$, 0.72 mg/L of $\text{CoCl}_2 \cdot 6\text{H}_2\text{O}$, 0.4 mg/L of boric acid, 1.2 mg/L of $\text{Na}_2\text{MoO}_4 \cdot 2\text{H}_2\text{O}$, 50 μ g/L of biotin, 50 μ g/L of calcium pantothenate, 50 μ g/L of folic acid, 50 μ g/L of inositol, 50 μ g/L of niacin, 50 μ g/L of p-aminobenzoic acid, 50 μ g/L of pyridoxine hydrochloride, 50 μ g/L of riboflavin, 50 μ g/L of thiamine hydrochloride, 50 mg/L of cycloheximide, 20 g/L of agar.

[0063] The media plated on which the above samples were plated were incubated at 28°C, 37°C or 50°C for 2 to 4 days and 378 strains each forming a colony were obtained.

[0064] Subsequently, each of the strains obtained as described above was inoculated in a test tube of 16.5 cm in length and 14 mm in diameter containing 3 mL of liquid medium (adjusted to pH 4.0 with HCl) containing a saturation concentration of L-glutamic acid and cultured at 28°C, 37°C or 50°C for 24 hours to 3 days with shaking. Then, the grown strains were selected. The composition of the aforementioned medium was as follows: 40 g/L of glucose, 20 g/L of $(\text{NH}_4)_2\text{SO}_4$, 0.5 g/L of $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 2 g/L of KH_2PO_4 , 0.5 g/L of NaCl, 0.25 g/L of $\text{CaCl}_2 \cdot 7\text{H}_2\text{O}$, 0.02 g/L of $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$, 0.02 g/L of $\text{MnSO}_4 \cdot 4\text{H}_2\text{O}$, 0.72 mg/L of $\text{ZnSO}_4 \cdot 2\text{H}_2\text{O}$, 0.64 mg/L of $\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$, 0.72 mg/L of $\text{CoCl}_2 \cdot 6\text{H}_2\text{O}$, 0.4 mg/L of boric acid, 1.2 mg/L of $\text{Na}_2\text{MoO}_4 \cdot 2\text{H}_2\text{O}$, 2 g/L of yeast extract.

[0065] Thus, 78 strains of microorganisms having L-glutamic acid resistance in an acidic environment were successfully obtained.

(2) Selection of strains with superior growth rate in acidic environment from microorganisms having L-glutamic acid resistance

[0066] The various microorganisms having L-glutamic acid resistance in an acidic environment obtained as described above were each inoculated into a test tube of 16.5 cm in length and 14 mm in diameter containing 3 mL of medium (adjusted to pH 4.0 with HCl) obtained by adding 20 g/L of glutamic acid and 2 g/L of glucose to M9 medium (Sambrook, J., Fritsch, E.F. and Maniatis, T., "Molecular Cloning", Cold Spring Harbor Laboratory Press, 1989), and the turbidity of the medium was measured in the time course to select strains with a favorable growth rate. As a result, as a strain showing favorable growth, the AJ13355 strain was obtained from a soil in Iwata-shi, Shizuoka, Japan. This strain was determined as *Enterobacter agglomerans* based on its bacteriological properties described above.

(3) Acquisition of strain with less viscous material secretion from *Enterobacter agglomerans* AJ13355 strain

[0067] Since the *Enterobacter agglomerans* AJ13355 strain extracellularly secretes a viscous material when cultured in a medium containing a saccharide, operation efficiency is not favorable. Therefore, a strain with less viscous material secretion was obtained by the ultraviolet irradiation method (Miller, J.H. et al., "A Short Course in Bacterial Genetics; Laboratory Manual", p.150, Cold Spring Harbor Laboratory Press, 1992).

[0068] The *Enterobacter agglomerans* AJ13355 strain was irradiated with ultraviolet ray for 2 minutes at the position 60 cm away from a 60-W ultraviolet lamp and cultured in LB medium overnight to fix mutation. The mutagenized strain was diluted and inoculated in LB medium containing 5 g/L of glucose and 20 g/L of agar so that about 100 colonies per plate would emerge and cultured at 30°C overnight with tilting the plate about 45 degrees, and then 20 colonies showing no flowing down of the viscous material were selected.

[0069] As a strain satisfying conditions that no revertant emerged even after 5 times of subculture in LB medium containing 5 g/L of glucose and 20 g/L of agar, and that there should be observed growth equivalent to the parent strain in LB medium, LB medium containing 5 g/L of glucose and M9 medium (Sambrook, J. et al., Molecular Cloning, 2nd Edition, Cold Spring Harbor Press, 1989) to which 20 g/L of L-glutamic acid and 2 g/L of glucose were added and of which pH was adjusted to 4.5 with HCl, SC17 strain was selected from the strains selected above.

(4) Construction of glutamic acid-producing bacterium from *Enterobacter agglomerans* SC17 strain(1) Preparation of α KGDH deficient strain from *Enterobacter agglomerans* SC17 strain

5 [0070] A strain deficient in α KGDH and with enhanced L-glutamic acid biosynthetic system was prepared from the *Enterobacter agglomerans* SC17 strain.

(i) Cloning of α KGDH gene (hereafter, referred to as "*sucAB*") of *Enterobacter agglomerans* AJ13355 strain

10 [0071] The *sucAB* gene of the *Enterobacter agglomerans* AJ13355 strain was cloned by selecting a DNA fragment complementing the acetic acid-unassimilating property of the α KGDH-E1 subunit gene (hereafter, referred to as "*sucA*") deficient strain of *Escherichia coli* from chromosomal DNA of the *Enterobacter agglomerans* AJ13355 strain.

[0072] The chromosomal DNA of the *Enterobacter agglomerans* AJ13355 strain was isolated by a method usually employed when chromosomal DNA is extracted from *Escherichia coli* (Text for Bioengineering Experiments, Edited by the Society for Bioscience and Bioengineering, Japan, pp.97-98, Baifukan, 1992). The pTWV228 (resistant to ampicillin) used as a vector was commercially available one from Takara Shuzo Co., Ltd.

[0073] The chromosomal DNA of the AJ13355 strain digested with *Eco*T221 and pTWV228 digested with *Pst*I were ligated by using T4 ligase and used to transform the *sucA* deficient *Escherichia coli* JRG465 strain (Herbert, J. et al., Mol. Gen. Genetics, 105, 182 (1969)). A strain growing in an acetate minimal medium was selected from the transformant strains obtained above, and a plasmid was extracted from it and designated as pTWVEK101. The *Escherichia coli* JRG465 strain harboring pTWVEK101 recovered auxotrophy for succinic acid or L-lysine and L-methionine besides the acetic acid-assimilating property. This suggests that pTWVEK101 contains the *sucA* gene of *Enterobacter agglomerans*.

[0074] Fig. 1 shows the restriction map of a DNA fragment derived from *Enterobacter agglomerans* in pTWVEK101. The determined nucleotide sequence of the hatched portion in Fig. 1 is shown as SEQ ID NO: 1. In this sequence, nucleotide sequences considered to be two full length ORFs and two nucleotide sequences considered to be partial sequences of the ORFs were found. SEQ ID NOS: 2 to 5 show amino acid sequences that can be encoded by these ORFs or partial sequences in an order from the 5' end. As a result of homology search for these, it was revealed that the portion of which nucleotide sequences were determined contained a 3'-end partial sequence of the succinate dehydrogenase iron-sulfur protein gene (*sdhB*), full length *sucA* and α KGDH-E2 subunit gene (*sucB*), and 5'-end partial sequence of the succinyl CoA synthetase β subunit gene (*sucC*). The results of comparison of the amino acid sequences deduced from these nucleotide sequences with those derived from *Escherichia coli* (Eur. J. Biochem., 141, pp.351-359 (1984); Eur. J. Biochem., 141, pp.361-374 (1984); Biochemistry, 24, pp.6245-6252 (1985)) are shown in Figs. 2 to 5. Thus, the amino acid sequences each showed very high homology. In addition, it was found that a cluster of *sdhB-sucA-sucB-sucC* was constituted on the chromosome of *Enterobacter agglomerans* as in *Escherichia coli* (Eur. J. Biochem., 141, pp.351-359 (1984); Eur. J. Biochem., 141, pp.361-374 (1984); Biochemistry, 24, pp.6245-6252 (1985)).

(ii) Acquisition of α KGDH deficient strain derived from *Enterobacter agglomerans* SC17 strain

40 [0075] The homologous recombination was performed by using the *sucAB* gene of *Enterobacter agglomerans* obtained as described above to obtain an α KGDH deficient strain of *Enterobacter agglomerans*.

[0076] After pTWVEK101 was digested with *Sph*I to excise a fragment containing *sucA*, the fragment was blunt-ended with Klenow fragment (Takara Shuzo Co., Ltd.) and ligated with pBR322 digested with *Eco*RI and blunt-ended with Klenow fragment, by using T4 DNA ligase (Takara Shuzo Co., Ltd.). The obtained plasmid was digested at the restriction enzyme *Bgl*II recognition site positioned substantially at the center of *sucA* by using this enzyme, blunt-ended with Klenow fragment, and then ligated again by using T4 DNA ligase. It was considered that the *sucA* gene did not function because a frameshift mutation was introduced into *sucA* of the plasmid newly constructed through the above procedure.

50 [0077] The plasmid constructed as described above was digested with a restriction enzyme *Apa*LI, and subjected to agarose gel electrophoresis to recover a DNA fragment containing *sucA* into which the frameshift mutation was introduced and a tetracycline resistance gene derived from pBR322. The recovered DNA fragment was ligated again by using T4 DNA ligase to construct a plasmid for disrupting the α KGDH gene.

[0078] The plasmid for disrupting the α KGDH gene obtained as described above was used to transform the *Enterobacter agglomerans* SC17 strain by electroporation (Miller, J.H., "A Short Course in Bacterial Genetics; Handbook", p.279, Cold Spring Harbor Laboratory Press, U.S.A., 1992), and a strain wherein *sucA* on the chromosome was replaced with a mutant type one by homologous recombination of the plasmid was obtained by using the tetracycline resistance as an indicator. The obtained strain was designated as SC17*sucA* strain.

[0079] In order to confirm that the SC17sucA strain was deficient in the α KGDH activity, the enzyme activity was measured by the method of Reed et al. (Reed, L.J. and Mukherjee, B.B., Methods in Enzymology, 13, pp.55-61, (1969)) by using cells of the strain cultured in LB medium until the logarithmic growth phase. As a result, α KGDH activity of 0.073 (Δ ABS/min/mg protein) was detected from the SC17 strain, whereas no α KGDH activity was detected from the SC17sucA strain, and thus it was confirmed that the *sucA* was deficient as purposed.

(2) Enhancement of L-glutamic acid biosynthetic system of *Enterobacter agglomerans* SC17sucA strain

[0080] Subsequently, a citrate synthase gene, a phosphoenolpyruvate carboxylase gene and a glutamate dehydrogenase gene derived from *Escherichia coli* were introduced into the SC17sucA strain.

(i) Preparation of plasmid having *gltA* gene, *ppc* gene and *gdhA* gene derived from *Escherichia coli*

[0081] The procedures of preparing a plasmid having a *gltA* gene, a *ppc* gene and a *gdhA* gene will be explained by referring to Figs. 6 and 7.

[0082] A plasmid having a *gdhA* gene derived from *Escherichia coli*, pBRGDH (Japanese Patent Application Laid-open No. 7-203980), was digested with *Hind*III and *Sph*I, the both ends were blunt-ended by the T4 DNA polymerase treatment, and then the DNA fragment having the *gdhA* gene was purified and recovered. Separately, a plasmid having a *gltA* gene and a *ppc* gene derived from *Escherichia coli*, pMWCP (WO 97/08294), was digested with *Xba*I, and then the both ends were blunt-ended by using T4 DNA polymerase. This was mixed with the above purified DNA fragment having the *gdhA* gene and ligated by using T4 ligase to obtain a plasmid pMWCPG, which corresponded to pMWCP further containing the *gdhA* gene (Fig. 6).

[0083] At the same time, the plasmid pVIC40 (Japanese Patent Application Laid-open No. 8-047397) having the replication origin of the broad host spectrum plasmid RSF1010 was digested with *Not*I, treated with T4 DNA polymerase and digested with *Pst*I. pBR322 was digested with *Eco*T14I, treated with T4 DNA polymerase and digested with *Pst*I. The both products were mixed and ligated by using T4 ligase to obtain a plasmid RSF-Tet having the replication origin of RSF1010 and a tetracycline resistance gene (Fig. 7).

[0084] Subsequently, pMWCPG was digested with *Eco*RI and *Pst*I, and a DNA fragment having the *gltA* gene, the *ppc* gene and the *gdhA* gene was purified and recovered. RSF-Tet was similarly digested with *Eco*RI and *Pst*I, and a DNA fragment having the replication origin of RSF1010 was purified and recovered. The both products were mixed and ligated by using T4 ligase to obtain a plasmid RSFCPG, which corresponded to RSF-Tet containing the *gltA* gene, the *ppc* gene and the *gdhA* gene (Fig. 8). It was confirmed that the obtained plasmid RSFCPG expressed the *gltA* gene, the *ppc* gene and the *gdhA* gene, by the complementation of the auxotrophy of the *gltA*, *ppc* or *gdhA* gene deficient strain derived from *Escherichia coli* and measurement of each enzyme activity.

(ii) Preparation of plasmid having *gltA* gene derived from *Brevibacterium lactofermentum*

[0085] A plasmid having the *gltA* gene derived from *Brevibacterium lactofermentum* was constructed as follows. PCR was performed by using the primer DNAs having the nucleotide sequences represented by SEQ ID NOS: 6 and 7, which were prepared based on the nucleotide sequence of the *Corynebacterium glutamicum gltA* gene (Microbiology, 140, pp.1817-1828 (1994)), and chromosomal DNA of *Brevibacterium lactofermentum* ATCC13869 as a template to obtain a *gltA* gene fragment of about 3 kb. This fragment inserted into a plasmid pHSG399 (purchased from Takara Shuzo Co., Ltd.) digested with *Sma*I to obtain a plasmid pHSGCB (Fig. 9). Subsequently, pHSGCB was digested with *Hind*III, and the excised *gltA* gene fragment of about 3 kb was inserted into a plasmid pSTV29 (purchased from Takara Shuzo Co., Ltd.) digested with *Hind*III to obtain a plasmid pSTVCB (Fig. 9). It was confirmed that the obtained plasmid pSTVCB expressed the *gltA* gene, by measuring the enzyme activity in the *Enterobacter agglomerans* AJ13355 strain.

(iii) Introduction of RSFCPG and pSTVCB into SC17sucA strain

[0086] The *Enterobacter agglomerans* SC17sucA strain was transformed with RSFCPG by electroporation to obtain a transformant SC17sucA/RSFCPG strain having tetracycline resistance. Further, the SC17sucA/RSFCPG strain was transformed with pSTVCB by electroporation to obtain a transformant SC17sucA/RSFCPG+pSTVCB strain having chloramphenicol resistance.

(4) Acquisition of strain with improved resistance to L-glutamic acid in low pH environment

[0087] A strain with improved resistance to L-glutamic acid at a high concentration in a low pH environment (hereafter, also referred to as "high-concentration Glu-resistant strain at low pH") was isolated from the *Enterobacter*

agglomerans SC17sucA/RSFCPG+pSTVCB strain.

[0088] The SC17sucA/RSFCPG+pSTVCB strain was cultured overnight at 30°C in LBG medium (10 g/L of tryptone, 5 g/L of yeast extract, 10 g/L of NaCl, 5 g/L of glucose), and the cells washed with saline was appropriately diluted and plated on an M9-E medium (4 g/L of glucose, 17 g/L of $\text{Na}_2\text{HPO}_4 \cdot 12\text{H}_2\text{O}$, 3 g/L of KH_2PO_4 , 0.5 g/L of NaCl, 1 g/L of NH_4Cl , 10 mM of MgSO_4 , 10 μM of CaCl_2 , 50 mg/L of L-lysine, 50 mg/L of L-methionine, 50 mg/L of DL-diaminopimelic acid, 25 mg/L of tetracycline, 25 mg/L of chloramphenicol, 30 g/L of L-glutamic acid, adjusted to pH 4.5 with aqueous ammonia) plate. The colony emerged after culture at 32°C for 2 days was obtained as a high-concentration Glu-resistant strain at low pH.

[0089] For the obtained strain, growth level in M9-E liquid medium was measured and L-glutamic acid-producing ability was tested in a 50-ml volume large test tube containing 5 ml of L-glutamic acid production test medium (40 g/L of glucose, 20 g/L of $(\text{NH}_4)_2\text{SO}_4$, 0.5 g/L of $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 2 g/L of KH_2PO_4 , 0.5 g/L of NaCl, 0.25 g/L of $\text{CaCl}_2 \cdot 7\text{H}_2\text{O}$, 0.02 g/L of $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$, 0.02 g/L of $\text{MnSO}_4 \cdot 4\text{H}_2\text{O}$, 0.72 mg/L of $\text{ZnSO}_4 \cdot 2\text{H}_2\text{O}$, 0.64 mg/L of $\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$, 0.72 mg/L of $\text{CoCl}_2 \cdot 6\text{H}_2\text{O}$, 0.4 mg/L of boric acid, 1.2 mg/L of $\text{Na}_2\text{MoO}_4 \cdot 2\text{H}_2\text{O}$, 2 g/L of yeast extract, 200 mg/L of L-lysine hydrochloride, 200 mg/L of L-methionine, 200 mg/L of DL- α,ϵ -diaminopimelic acid, 25 mg/L of tetracycline hydrochloride, 25 mg/L of chloramphenicol). A strain that exhibited the best growth level and the same L-glutamic acid producing ability as that of its parent strain, the SC17/RSFCPG+pSTVCB strain, was designated as *Enterobacter agglomerans* AJ13601. The AJ13601 strain was deposited at the National Institute of Bioscience and Human-Technology, Agency of Industrial Science and Technology, Ministry of International Trade and Industry (postal code: 305-8566, 1-3, Higashi 1-chome, Tsukuba-shi, Ibaraki, Japan) on August 18, 1999 and received an accession number of FERM P-17516. It was then transferred to an international deposition under the provisions of Budapest Treaty on July 6, 2000 and received an accession number of FERM BP-7207.

(5) Culture of *Enterobacter agglomerans* AJ13601 strain for L-glutamic acid production (1)

[0090] The *Enterobacter agglomerans* AJ13601 strain was inoculated into a 1-L jar fermenter containing 300 ml of medium containing 40 g/L of glucose, 20 g/L of $(\text{NH}_4)_2\text{SO}_4$, 0.5 g/L of $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 2 g/L of KH_2PO_4 , 0.5 g/L of NaCl, 0.25 g/L of $\text{CaCl}_2 \cdot 7\text{H}_2\text{O}$, 0.02 g/L of $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$, 0.02 g/L of $\text{MnSO}_4 \cdot 4\text{H}_2\text{O}$, 0.72 mg/L of $\text{ZnSO}_4 \cdot 2\text{H}_2\text{O}$, 0.64 mg/L of $\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$, 0.72 mg/L of $\text{CoCl}_2 \cdot 6\text{H}_2\text{O}$, 0.4 mg/L of boric acid, 1.2 mg/L of $\text{Na}_2\text{MoO}_4 \cdot 2\text{H}_2\text{O}$, 2 g/L of yeast extract, 200 mg/L of L-lysine hydrochloride, 200 mg/L of L-methionine, 200 mg/L of DL- α,ϵ -diaminopimelic acid, 25 mg/L of tetracycline hydrochloride and 25 mg/L of chloramphenicol, and cultured at 34°C and pH 6.0 for 14 hours. The culture pH was controlled by introducing ammonia gas into the medium.

[0091] The culture obtained as described above was centrifuged at 5000 rpm for 10 minutes, and the collected cells were inoculated into a 1-L jar fermenter containing 300 ml of medium containing 40 g/L of glucose, 5 g/L of $(\text{NH}_4)_2\text{SO}_4$, 1.5 g/L of $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 6 g/L of KH_2PO_4 , 1.5 g/L of NaCl, 0.75 g/L of $\text{CaCl}_2 \cdot 7\text{H}_2\text{O}$, 0.06 g/L of $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$, 0.06 g/L of $\text{MnSO}_4 \cdot 4\text{H}_2\text{O}$, 2.16 mg/L of $\text{ZnSO}_4 \cdot 2\text{H}_2\text{O}$, 1.92 mg/L of $\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$, 2.16 mg/L of $\text{CoCl}_2 \cdot 6\text{H}_2\text{O}$, 1.2 mg/L of boric acid, 3.6 mg/L of $\text{Na}_2\text{MoO}_4 \cdot 2\text{H}_2\text{O}$, 6 g/L of yeast extract, 600 mg/L of L-lysine hydrochloride, 600 mg/L of L-methionine, 600 mg/L of DL- α,ϵ -diaminopimelic acid, 25 mg/L of tetracycline hydrochloride and 25 mg/L of chloramphenicol and cultured at 34°C and pH 4.5 to perform culture for L-glutamic acid production. The culture pH was controlled by introducing ammonia gas into the medium. As the initially added glucose was depleted, 600 g/L of glucose was continuously added.

[0092] As a result of the culture for L-glutamic acid production performed for 50 hours as described above, a substantial amount of L-glutamic acid crystals were precipitated in the jar fermenter. Table 1 shows the concentration of L-glutamic acid dissolved in the culture broth at that time and the L-glutamic acid concentration measured by dissolving the crystals in 2 M potassium hydroxide. L-Glutamic acid crystals were collected from the culture by decantation after the culture was left stood.

Table 1

Concentration of L-glutamic acid dissolved in culture broth	51 g/L
Amount of L-glutamic acid precipitated as crystals	67 g/L
Concentration of L-glutamic acid measured by dissolving crystals	118 g/L

(6) Culture of *Enterobacter agglomerans* AJ13601 strain for L-glutamic acid production (2)

[0093] The following experiment was performed in order to confirm that the *Enterobacter agglomerans* AJ13601 strain still had L-glutamic acid-producing ability even under the condition that L-glutamic acid crystals were present.

[0094] The *Enterobacter agglomerans* AJ13601 strain was inoculated into a 1-L jar fermenter containing 300 ml of medium containing 40 g/L of glucose, 20 g/L of $(\text{NH}_4)_2\text{SO}_4$, 0.5 g/L of $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 2 g/L of KH_2PO_4 , 0.5 g/L of NaCl, 0.25 g/L of $\text{CaCl}_2 \cdot 7\text{H}_2\text{O}$, 0.02 g/L of $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$, 0.02 g/L of $\text{MnSO}_4 \cdot 4\text{H}_2\text{O}$, 0.72 mg/L of $\text{ZnSO}_4 \cdot 2\text{H}_2\text{O}$, 0.64 mg/L of $\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$, 0.72 mg/L of $\text{CoCl}_2 \cdot 6\text{H}_2\text{O}$, 0.4 mg/L of boric acid, 1.2 mg/L of $\text{Na}_2\text{MoO}_4 \cdot 2\text{H}_2\text{O}$, 2 g/L of yeast extract, 200 mg/L of L-lysine hydrochloride, 200 mg/L of L-methionine, 200 mg/L of DL- α,ϵ -diaminopimelic acid, 25 mg/L of tetracycline hydrochloride and 25 mg/L of chloramphenicol, and cultured at 34°C at pH 6.0 for 14 hours. The culture pH was controlled by bubbling the medium with ammonia gas. The culture obtained as described above was centrifuged at 5000 rpm for 10 minutes, and then the collected cells were cultured in a medium where L-glutamic acid was present as crystals. The used medium contained 40 g/L of glucose, 5 g/L of $(\text{NH}_4)_2\text{SO}_4$, 1.5 g/L of $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 6 g/L of KH_2PO_4 , 1.5 g/L of NaCl, 0.75 g/L of $\text{CaCl}_2 \cdot 7\text{H}_2\text{O}$, 0.06 g/L of $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$, 0.06 g/L of $\text{MnSO}_4 \cdot 4\text{H}_2\text{O}$, 2.16 mg/L of $\text{ZnSO}_4 \cdot 2\text{H}_2\text{O}$, 1.92 mg/L of $\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$, 2.16 mg/L of $\text{CoCl}_2 \cdot 6\text{H}_2\text{O}$, 1.2 mg/L of boric acid, 3.6 mg/L of $\text{Na}_2\text{MoO}_4 \cdot 2\text{H}_2\text{O}$, 6 g/L of yeast extract, 600 mg/L of L-lysine hydrochloride, 600 mg/L of L-methionine, 600 mg/L of DL- α,ϵ -diaminopimelic acid, 25 mg/L of tetracycline hydrochloride and 25 mg/L of chloramphenicol and L-glutamic acid crystals were added to 40 g/L. The cells were inoculated in a 1-L jar fermenter containing 300 ml of this medium and cultured at 34°C and pH 4.3 to perform culture for L-glutamic acid production. The culture pH was controlled by introducing ammonia gas into the medium. As the initially added glucose was depleted, 600 g/L of glucose was continuously added. In this medium, only 39 g/L of the added L-glutamic acid was dissolved at pH 4.3 and the remaining 1 g/L was present as crystals.

[0095] As a result of the culture for L-glutamic acid production performed for 53 hours as described above, a substantial amount of L-glutamic acid crystals were precipitated in the jar fermenter. Table 2 shows the concentration of L-glutamic acid dissolved in the culture broth, the amount of L-glutamic acid present as crystals at that time and the L-glutamic acid concentration measured by dissolving the crystals in 2 M KOH solution. L-Glutamic acid crystals were collected from the culture by decantation after the culture was left stood. The results showed that the *Enterobacter agglomerans* AJ13601 strain accumulated L-glutamic acid and precipitated crystals thereof even under the condition that L-glutamic acid crystals were present.

Table 2

Concentration of L-glutamic acid dissolved in culture broth	39 g/L
Amount of L-glutamic acid precipitated as crystals	119 g/L
Concentration of L-glutamic acid measured by dissolving crystals	158 g/L
Amount of L-glutamic acid crystals newly produced by main culture	118 g/L

(7) Culture of *Enterobacter agglomerans* AJ13601 strain for L-glutamic acid production (3)

[0096] The *Enterobacter agglomerans* AJ13601 strain can grow not only at an acidic pH, but also at a neutral pH. Therefore, it was confirmed as follows that L-glutamic acid crystals could also be precipitated by starting the culture at a neutral pH and allowing production of L-glutamic acid during the culture so that pH of the culture should spontaneously be lowered.

[0097] Cells of one plate (8.5 cm in diameter) of the *Enterobacter agglomerans* AJ13601 strain, cultured on LBG agar medium (10 g/L of L tryptone, 5 g/L of yeast extract, 10 g/L of NaCl, 5 g/L of glucose, 15 g/L of agar) containing 25 mg/L of tetracycline hydrochloride and 25 mg/L of chloramphenicol at 30°C for 14 hours, were inoculated into a 1-L jar fermenter containing 300 ml of medium containing 40 g/L of glucose, 5 g/L of $(\text{NH}_4)_2\text{SO}_4$, 1.5 g/L of $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 6 g/L of KH_2PO_4 , 1.5 g/L of NaCl, 0.75 g/L of $\text{CaCl}_2 \cdot 7\text{H}_2\text{O}$, 0.06 g/L of $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$, 0.06 g/L of $\text{MnSO}_4 \cdot 4\text{H}_2\text{O}$, 2.16 mg/L of $\text{ZnSO}_4 \cdot 2\text{H}_2\text{O}$, 1.92 mg/L of $\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$, 2.16 mg/L of $\text{CoCl}_2 \cdot 6\text{H}_2\text{O}$, 1.2 mg/L of boric acid, 3.6 mg/L of $\text{Na}_2\text{MoO}_4 \cdot 2\text{H}_2\text{O}$, 6 g/L of yeast extract, 600 mg/L of L-lysine hydrochloride, 600 mg/L of L-methionine, 600 mg/L of DL- α,ϵ -diaminopimelic acid, 25 mg/L of tetracycline hydrochloride and 25 mg/L of chloramphenicol and the culture was started at 34°C and pH 7.0. The culture pH was controlled by introducing ammonia gas into the medium. As the initially added glucose was depleted, 600 g/L of glucose was continuously added.

[0098] As L-glutamic acid is accumulated, pH lowers spontaneously. The amount of the introduced ammonia gas was adjusted so that pH should be gradually lowered from 7.0 to 4.5 during the period between 15 hours and 24 hours after the start of the culture, and 24 hours after the start of the culture, pH became 4.5. Afterward, cultivation was continued for 12 hours.

[0099] As a result of the culture for L-glutamic acid production conducted for 36 hours as described above, a substantial amount of L-glutamic acid crystals were precipitated in the jar fermenter. Table 3 shows the concentration of L-glutamic acid dissolved in the culture broth, the amount of L-glutamic acid present as crystals at that time and the L-

EP 1 078 989 A2

glutamic acid concentration measured by dissolving the crystals in 2 M KOH solution. L-Glutamic acid crystals were collected from the culture by decantation after the culture was left stood.

Tabl 3

Concentration of L-glutamic acid dissolved in cultur broth	45 g/L
Amount of L-glutamic acid precipitated as crystals	31 g/L
Concentration of L-glutamic acid measured by dissolving crystals	76 g/L

SEQUENCE LISTING

5 <110> Ajinomoto Co., Inc.

<120> Method for producing L-glutamic acid by fermentation accompanied by precipitation

10 <130>

<150> JP 11-234806
<151> 1999-08-20

15 <150> JP 2000-78771
<151> 2000-03-21

<160> 7

20 <170> PatentIn Ver. 2.0

<210> 1
<211> 4556
<212> DNA
25 <213> Enterobacter agglomerans

<220>
<221> CDS
30 <222> (2)..(121)

<220>
<221> CDS
35 <222> (322)..(3129)

<220>
<221> CDS
40 <222> (4437)..(4556)

<400> 1

45 t gca ttc agc gtt ttc cgc tgt cac agc atc atg aac tgt gta agt gtt 49
Ala Phe Ser Val Phe Arg Cys His Ser Ile Met Asn Cys Val Ser Val
1 5 10 15
tgt cct aaa ggg cta aac ccg acg cgc gct atc ggc cac att aag tcg 97
Cys Pro Lys Gly Leu Asn Pro Thr Arg Ala Ile Gly His Ile Lys Ser
50 20 25 30
atg ctg ctg caa cgc agc gcg tagttatacc accgggaacc tcaggttccc 148
Met Leu Leu Gln Arg Ser Ala

55

55

	ctg ggg atg gcg cac cgt ggc cgt ctt aac gta ctg att aac gta ctg	1140
	Leu Gly Met Ala His Arg Gly Arg Leu Asn Val Leu Ile Asn Val Leu	
	260 265 270	
5	ggt aaa aag cca cag gat ctg ttc gac gaa ttc tcc ggt aaa cac aaa	1188
	Gly Lys Lys Pro Gln Asp Leu Phe Asp Glu Phe Ser Gly Lys His Lys	
	275 280 285	
	gag cat ctg ggc acc ggt gat gtg aag tat cac atg ggc ttc tct tcg	1236
	Glu His Leu Gly Thr Gly Asp Val Lys Tyr His Met Gly Phe Ser Ser	
10	290 295 300 305	
	gat att gaa acc gaa ggt ggt ctg gtg cat ctg gcg ctg gcg ttt aac	1284
	Asp Ile Glu Thr Glu Gly Gly Leu Val His Leu Ala Leu Ala Phe Asn	
	310 315 320	
	ccg tct cac ctg gaa att gtc agc ccg gtg gtc atg gga tgc gta cgt	1332
15	Pro Ser His Glu Ile Val Ser Pro Val Val Met Gly Ser Val Arg	
	325 330 335	
	gca cgt ctc gat cgt ctg gcc gaa ccg gtc agc aat aaa gtg ttg cct	1380
	Ala Arg Leu Asp Arg Leu Ala Glu Pro Val Ser Asn Lys Val Leu Pro	
	340 345 350	
	atc acc att cac ggt gat gcg gcg gtg att ggt cag ggc gtg gtt cag	1428
20	Ile Thr Ile His Gly Asp Ala Ala Val Ile Gly Gln Gly Val Val Gln	
	355 360 365	
	gaa acc ctg aac atg tct cag gcg gcg ggc tac gaa gtg ggc ggc acg	1476
	Glu Thr Leu Asn Met Ser Gln Ala Arg Gly Tyr Glu Val Gly Gly Thr	
	370 375 380 385	
25	gta cgt atc gtc att aac aac cag gtt ggt ttt acc acc tcc aac ccg	1524
	Val Arg Ile Val Ile Asn Asn Gln Val Gly Phe Thr Thr Ser Asn Pro	
	390 395 400	
	aaa gat gcg cgt tca acc ccg tac tgt act gac atc ggc aag atg gtg	1572
	Lys Asp Ala Arg Ser Thr Pro Tyr Cys Thr Asp Ile Gly Lys Met Val	
	405 410 415	
30	ctg gca ccg att ttc cac gtc aat gct gac gat ccg gaa gcg gtg gcc	1620
	Leu Ala Pro Ile Phe His Val Asn Ala Asp Asp Pro Glu Ala Val Ala	
	420 425 430	
	ttt gtt acc cgc ctg gcg ctg gac tat cgc aac acc ttc aaa cgc gat	1668
	Phe Val Thr Arg Leu Ala Leu Asp Tyr Arg Asn Thr Phe Lys Arg Asp	
35	435 440 445	
	gtg ttt atc gat ctg gtg tgc tat cgc cgt cat ggt cac aac gag gcg	1716
	Val Phe Ile Asp Leu Val Cys Tyr Arg Arg His Gly His Asn Glu Ala	
	450 455 460 465	
	gat gag cca agt gct acc cag ccg ttg atg tac cag aaa atc aaa aag	1764
40	Asp Glu Pro Ser Ala Thr Gln Pro Leu Met Tyr Gln Lys Ile Lys Lys	
	470 475 480	
	cat ccg acg ccg cgt aaa att tac gcc gat cgt ctg gaa ggc gaa ggt	1812
	His Pro Thr Pro Arg Lys Ile Tyr Ala Asp Arg Leu Glu Gly Glu Gly	
	485 490 495	
45	gtc gcg tgc cag gaa gat gcc acc gag atg gtg aac ctg tac cgc gat	1860
	Val Ala Ser Gln Glu Asp Ala Thr Glu Met Val Asn Leu Tyr Arg Asp	
	500 505 510	
	gcg ctc gat gcg ggc gaa tgc gtg gtg ccg gaa tgg cgt ccg atg agc	1908
	Ala Leu Asp Ala Gly Glu Cys Val Val Pro Glu Trp Arg Pro Met Ser	
	515 520 525	
50	ctg cac tcc ttc acg tgg tgc cct tat ctg aac cac gaa tgg gat gag	1956
	Leu His Ser Phe Thr Trp Ser Pro Tyr Leu Asn His Glu Trp Asp Glu	
	530 535 540 545	

55

	cct tat ccg gca cag gtt gac atg aaa cgc ctg aag gaa ctg gca ttg	2004
	Pro Tyr Pro Ala Gln Val Asp Met Lys Arg Leu Lys Glu Leu Ala Leu	
	550 555 560	
5	cgt atc agc cag gtc cct gag cag att gaa gtg cag tcg cgc gtg gcc	2052
	Arg Ile Ser Gln Val Pro Glu Gln Ile Glu Val Gln Ser Arg Val Ala	
	565 570 575	
	aag atc tat aac gat cgc aag ctg atg gcc gaa ggc gag aaa gcg ttc	2100
	Lys Ile Tyr Asn Asp Arg Lys Leu Met Ala Glu Gly Glu Lys Ala Phe	
10	580 585 590	
	gac tgg ggc ggt gcc gag aat ctg gcg tac gcc acg ctg gtg gat gaa	2148
	Asp Trp Gly Gly Ala Glu Asn Leu Ala Tyr Ala Thr Leu Val Asp Glu	
	595 600 605	
	ggt att ccg gtt cgc ctc tcg ggt gaa gac tcc ggt cgt gga acc ttc	2196
15	Gly Ile Pro Val Arg Leu Ser Gly Glu Asp Ser Gly Arg Gly Thr Phe	
	610 615 620 625	
	ttc cat cgc cac gcg gtc gtg cac aac cag gct aac ggt tca acc tat	2244
	Phe His Arg His Ala Val Val His Asn Gln Ala Asn Gly Ser Thr Tyr	
	630 635 640	
	acg ccg ctg cac cat att cat aac agc cag ggc gag ttc aaa gtc tgg	2292
20	Thr Pro Leu His His Ile His Asn Ser Gln Gly Glu Phe Lys Val Trp	
	645 650 655	
	gat tcg gtg ctg tct gaa gaa gcg gtg ctg gcg ttt gaa tac ggt tac	2340
	Asp Ser Val Leu Ser Glu Glu Ala Val Leu Ala Phe Glu Tyr Gly Tyr	
	660 665 670	
25	gcc acg gct gag ccg cgc gtg ctg acc atc tgg gaa gcg cag ttt ggt	2388
	Ala Thr Ala Glu Pro Arg Val Leu Thr Ile Trp Glu Ala Gln Phe Gly	
	675 680 685	
	gac ttt gcc aac ggt gct cag gtg gtg att gac cag ttc atc agc tct	2436
	Asp Phe Ala Asn Gly Ala Gln Val Val Ile Asp Gln Phe Ile Ser Ser	
	690 695 700 705	
30	ggc gaa cag aag tgg ggc cgt atg tgt ggc ctg gtg atg ttg ctg ccg	2484
	Gly Glu Gln Lys Trp Gly Arg Met Cys Gly Leu Val Met Leu Leu Pro	
	710 715 720	
	cat ggc tac gaa ggt cag gga ccg gaa cac tcc tct gcc cgt ctg gaa	2532
35	His Gly Tyr Glu Gly Gln Gly Pro Glu His Ser Ser Ala Arg Leu Glu	
	725 730 735	
	cgc tat ctg caa ctt tgc gcc gag cag aac atg cag gtt tgc gtc ccg	2580
	Arg Tyr Leu Gln Leu Cys Ala Glu Gln Asn Met Gln Val Cys Val Pro	
	740 745 750	
	tcg acg ccg gct cag gtg tat cac atg ctg cgc cgt cag gcg ctg cgc	2628
40	Ser Thr Pro Ala Gln Val Tyr His Met Leu Arg Arg Gln Ala Leu Arg	
	755 760 765	
	ggg atg cgc cgt ccg ctg gtg gtg atg tcg ccg aag tcg ctg tta cgc	2676
	Gly Met Arg Arg Pro Leu Val Val Met Ser Pro Lys Ser Leu Leu Arg	
	770 775 780 785	
	cat cca ctg gcg atc tcg tcg ctg gat gaa ctg gca aac ggc agt ttc	2724
45	His Pro Leu Ala Ile Ser Ser Leu Asp Glu Leu Ala Asn Gly Ser Phe	
	790 795 800	
	cag ccg gcc att ggt gag atc gac gat ctg gat ccg cag ggc gtg aaa	2772
	Gln Pro Ala Ile Gly Glu Ile Asp Asp Leu Asp Pro Gln Gly Val Lys	
	805 810 815	
50	cgc gtc gtg ctg tgc tcc ggt aag gtt tac tac gat ctg ctg gaa cag	2820
	Arg Val Val Leu Cys Ser Gly Lys Val Tyr Tyr Asp Leu Leu Glu Gln	
	820 825 830	

55

	cgt cgt aaa gac gag aaa acc gat gtt gcc atc gtg cgc atc gaa cag	2868
	Arg Arg Lys Asp Glu Lys Thr Asp Val Ala Ile Val Arg Ile Glu Gln	
	835 840 845	
5	ctt tac ccg ttc ccg cat cag gcg gta cag gaa gca ttg aaa gcc tat	2916
	Leu Tyr Pro Phe Pro His Gln Ala Val Gln Glu Ala Leu Lys Ala Tyr	
	850 855 860 865	
	tct cac gta cag gac ttt gtc tgg tgc cag gaa gag cct ctg aac cag	2964
	Ser His Val Gln Asp Phe Val Trp Cys Gln Glu Glu Pro Leu Asn Gln	
10	870 875 880	
	ggc gcc tgg tac tgt agc cag cat cat ttc cgt gat gtc gtg ccg ttt	3012
	Gly Ala Trp Tyr Cys Ser Gln His His Phe Arg Asp Val Val Pro Phe	
	885 890 895	
	ggg gcc acc ctg cgt tat gca ggt cgc ccg gca tgc gct tct ccg gcc	3060
15	Gly Ala Thr Leu Arg Tyr Ala Gly Arg Pro Ala Ser Ala Ser Pro Ala	
	900 905 910	
	gtg ggt tat atg tcc gta cac caa caa cag cag caa gac ctg gtt aat	3108
	Val Gly Tyr Met Ser Val His Gln Gln Gln Gln Gln Asp Leu Val Asn	
	915 920 925	
	gac gca ctg aac gtc aat taattaaaag gaaagata atg agt agc gta gat	3159
20	Asp Ala Leu Asn Val Asn Met Ser Ser Val Asp	
	930 935 1 5	
	att ctc gtt ccc gac ctg cct gaa tgc gtt gca gat gcc aca gta gca	3207
	Ile Leu Val Pro Asp Leu Pro Glu Ser Val Ala Asp Ala Thr Val Ala	
	10 15 20	
25	acc tgg cac aag aaa cca ggc gat gca gtc agc cgc gat gaa gtc atc	3255
	Thr Trp His Lys Lys Pro Gly Asp Ala Val Ser Arg Asp Glu Val Ile	
	25 30 35	
	gtc gaa att gaa act gac aaa gtc gtg ctg gaa gtg ccg gca tct gcc	3303
	Val Glu Ile Glu Thr Asp Lys Val Val Leu Glu Val Pro Ala Ser Ala	
	40 45 50	
30	gat ggc gtg ctg gaa gcc gtg ctg gaa gac gaa ggg gca acc gtt acg	3351
	Asp Gly Val Leu Glu Ala Val Leu Glu Asp Glu Gly Ala Thr Val Thr	
	55 60 65	
	tcc cgc cag atc ctg ggt cgc ctg aaa gaa ggc aac agt gcg ggt aaa	3399
	Ser Arg Gln Ile Leu Glu Arg Leu Lys Glu Gly Asn Ser Ala Gly Lys	
35	70 75 80 85	
	gaa agc agt gcc aaa gcg gaa agc aat gac acc acg cca gcc cag cgt	3447
	Glu Ser Ser Ala Lys Ala Glu Ser Asn Asp Thr Thr Pro Ala Gln Arg	
	90 95 100	
	cag aca gcg tgc ctt gaa gaa gag agc agc gat gcg ctc agc ccg gcg	3495
40	Gln Thr Ala Ser Leu Glu Glu Glu Ser Ser Asp Ala Leu Ser Pro Ala	
	105 110 115	
	atc cgt cgc ctg att gcg gag cat aat ctt gac gct gcg cag atc aaa	3543
	Ile Arg Arg Leu Ile Ala Glu His Asn Leu Asp Ala Ala Gln Ile Lys	
	120 125 130	
	ggc acc ggc gta ggc gga cgt tta acg cgt gaa gac gtt gaa aaa cat	3591
45	Gly Thr Gly Val Gly Gly Arg Leu Thr Arg Glu Asp Val Glu Lys His	
	135 140 145	
	ctg gcg aac aaa ccg cag gct gag aaa gcc gcc gcg cca gcg gcg ggt	3639
	Leu Ala Asn Lys Pro Gln Ala Glu Lys Ala Ala Ala Pro Ala Ala Gly	
	150 155 160 165	
50	gca gca acg gct cag cag cct gtt gcc aac cgc agc gaa aaa cgt gtt	3687
	Ala Ala Thr Ala Gln Gln Pro Val Ala Asn Arg Ser Glu Lys Arg Val	
	170 175 180	

55

	ccg atg acg cgt tta cgt aag cgc gtc gcg gag cgt ctg ctg gaa gcc	3735
	Pro Met Thr Arg Leu Arg Lys Arg Val Ala Glu Arg Leu Leu Glu Ala	
	185 190 195	
5	aag aac agc acc gcc atg ttg acg acc ttc aac gaa atc aac atg aag	3783
	Lys Asn Ser Thr Ala Met Leu Thr Phe Asn Glu Ile Asn Met Lys	
	200 205 210	
	ccg att atg gat ctg cgt aag cag tac gcc gat gcg ttc gag aag cgt	3831
	Pro Ile Met Asp Leu Arg Lys Gln Tyr Gly Asp Ala Phe Glu Lys Arg	
10	215 220 225	
	cac ggt gtg cgt ctg gcc ttt atg tct ttc tac atc aag gcc gtg gtc	3879
	His Gly Val Arg Leu Gly Phe Met Ser Phe Tyr Ile Lys Ala Val Val	
	230 235 240 245	
	gaa gcg ctg aag cgt tat cca gaa gtc aac gcc tct atc gat gcc gaa	3927
15	Glu Ala Leu Lys Arg Tyr Pro Glu Val Asn Ala Ser Ile Asp Gly Glu	
	250 255 260	
	gac gtg gtg tac cac aac tat ttc gat gtg agt att gcc gtc tct acg	3975
	Asp Val Val Tyr His Asn Tyr Phe Asp Val Ser Ile Ala Val Ser Thr	
	265 270 275	
	cca cgc gga ctg gtg acg cct gtc ctg cgt gac gtt gat gcg ctg agc	4023
20	Pro Arg Gly Leu Val Thr Pro Val Leu Arg Asp Val Asp Ala Leu Ser	
	280 285 290	
	atg gct gac atc gag aag aaa att aaa gaa ctg gca gtg aaa gcc cgt	4071
	Met Ala Asp Ile Glu Lys Lys Ile Lys Glu Leu Ala Val Lys Gly Arg	
	295 300 305	
25	gac gcc aag ctg acg gtt gac gat ctg acg gcc ggt aac ttt acc atc	4119
	Asp Gly Lys Leu Thr Val Asp Asp Leu Thr Gly Gly Asn Phe Thr Ile	
	310 315 320 325	
	acc aac ggt ggt gtg ttc ggt tgc ctg atg tct acg cca atc atc aac	4167
	Thr Asn Gly Gly Val Phe Gly Ser Leu Met Ser Thr Pro Ile Ile Asn	
	330 335 340	
30	ccg cca cag agc gcg att ctg gcc atg cac gcc att aaa gat cgt cct	4215
	Pro Pro Gln Ser Ala Ile Leu Gly Met His Ala Ile Lys Asp Arg Pro	
	345 350 355	
	atg gcg gtc aat ggt cag gtt gtg atc ctg cca atg atg tac ctg gct	4263
35	Met Ala Val Asn Gly Gln Val Val Ile Leu Pro Met Met Tyr Leu Ala	
	360 365 370	
	ctc tcc tac gat cac cgt tta atc gat ggt cgt gaa tct gtc gcc tat	4311
	Leu Ser Tyr Asp His Arg Leu Ile Asp Gly Arg Glu Ser Val Gly Tyr	
	375 380 385	
	ctg gtc gcg gtg aaa gag atg ctg gaa gat ccg gcg cgt ctg ctg ctg	4359
40	Leu Val Ala Val Lys Glu Met Leu Glu Asp Pro Ala Arg Leu Leu Leu	
	390 395 400 405	
	gat gtc tgattcatca ctgggcacgc gttgcgtgcc caatctcaat actcttttca	4415
	Asp Val	
	gatctgaatg gatagaacat c atg aac tta cac gaa tac cag gct aaa cag	4466
45	Met Asn Leu His Glu Tyr Gln Ala Lys Gln	
	1 5 10	
	ctg ttt gca cgg tat gcc atg cca gca ccg acc gcc tac gcc tgt act	4514
	Leu Phe Ala Arg Tyr Gly Met Pro Ala Pro Thr Gly Tyr Ala Cys Thr	
	15 20 25	
50	aca cca cgt gaa gca gaa gaa gcg gca tgc aaa atc ggt gca	4556
	Thr Pro Arg Glu Ala Glu Glu Ala Ala Ser Lys Ile Gly Ala	
	30 35 40	

55

<210> 2
 <211> 39
 <212> PRT
 <213> Enterobacter agglomerans

<400> 2
 Ala Phe Ser Val Phe Arg Cys His Ser Ile Met Asn Cys Val Ser Val
 1 5 10 15
 Cys Pro Lys Gly Leu Asn Pro Thr Arg Ala Ile Gly His Ile Lys Ser
 20 25 30
 Met Leu Leu Gln Arg Ser Ala
 35

<210> 3
 <211> 935
 <212> PRT
 <213> Enterobacter agglomerans

<400> 3
 Met Gln Asn Ser Ala Met Lys Pro Trp Leu Asp Ser Ser Trp Leu Ala
 1 5 10 15
 Gly Ala Asn Gln Ser Tyr Ile Glu Gln Leu Tyr Glu Asp Phe Leu Thr
 20 25 30
 Asp Pro Asp Ser Val Asp Ala Val Trp Arg Ser Met Phe Gln Gln Leu
 35 40 45
 Pro Gly Thr Gly Val Lys Pro Glu Gln Phe His Ser Ala Thr Arg Glu
 50 55 60
 Tyr Phe Arg Arg Leu Ala Lys Asp Ala Ser Arg Tyr Thr Ser Ser Val
 65 70 75 80
 Thr Asp Pro Ala Thr Asn Ser Lys Gln Val Lys Val Leu Gln Leu Ile
 85 90 95
 Asn Ala Phe Arg Phe Arg Gly His Gln Glu Ala Asn Leu Asp Pro Leu
 100 105 110
 Gly Leu Trp Lys Gln Asp Arg Val Ala Asp Leu Asp Pro Ala Phe His
 115 120 125
 Asp Leu Thr Asp Ala Asp Phe Gln Glu Ser Phe Asn Val Gly Ser Phe
 130 135 140
 Ala Ile Gly Lys Glu Thr Met Lys Leu Ala Asp Leu Phe Asp Ala Leu
 145 150 155 160
 Lys Gln Thr Tyr Cys Gly Ser Ile Gly Ala Glu Tyr Met His Ile Asn
 165 170 175
 Asn Thr Glu Glu Lys Arg Trp Ile Gln Gln Arg Ile Glu Ser Gly Ala
 180 185 190
 Ser Gln Thr Ser Phe Ser Gly Glu Glu Lys Lys Gly Phe Leu Lys Glu
 195 200 205
 Leu Thr Ala Ala Glu Gly Leu Glu Lys Tyr Leu Gly Ala Lys Phe Pro
 210 215 220
 Gly Ala Lys Arg Phe Ser Leu Glu Gly Gly Asp Ala Leu Val Pro Met
 225 230 235 240
 Leu Arg Glu Met Ile Arg His Ala Gly Lys Ser Gly Thr Arg Glu Val
 245 250 255
 Val Leu Gly Met Ala His Arg Gly Arg Leu Asn Val Leu Ile Asn Val
 260 265 270

Leu Gly Lys Lys Pro Gln Asp Leu Phe Asp Glu Phe Ser Gly Lys His
 275 280 285
 Lys Glu His Leu Gly Thr Gly Asp Val Lys Tyr His Met Gly Phe Ser
 290 295 300
 Ser Asp Ile Glu Thr Glu Gly Gly Leu Val His Leu Ala Leu Ala Phe
 305 310 315 320
 Asn Pro Ser His Leu Glu Ile Val Ser Pro Val Val Met Gly Ser Val
 325 330 335
 Arg Ala Arg Leu Asp Arg Leu Ala Glu Pro Val Ser Asn Lys Val Leu
 340 345 350
 Pro Ile Thr Ile His Gly Asp Ala Ala Val Ile Gly Gln Gly Val Val
 355 360 365
 Gln Glu Thr Leu Asn Met Ser Gln Ala Arg Gly Tyr Glu Val Gly Gly
 370 375 380
 Thr Val Arg Ile Val Ile Asn Asn Gln Val Gly Phe Thr Thr Ser Asn
 385 390 395 400
 Pro Lys Asp Ala Arg Ser Thr Pro Tyr Cys Thr Asp Ile Gly Lys Met
 405 410 415
 Val Leu Ala Pro Ile Phe His Val Asn Ala Asp Asp Pro Glu Ala Val
 420 425 430
 Ala Phe Val Thr Arg Leu Ala Leu Asp Tyr Arg Asn Thr Phe Lys Arg
 435 440 445
 Asp Val Phe Ile Asp Leu Val Cys Tyr Arg Arg His Gly His Asn Glu
 450 455 460
 Ala Asp Glu Pro Ser Ala Thr Gln Pro Leu Met Tyr Gln Lys Ile Lys
 465 470 475 480
 Lys His Pro Thr Pro Arg Lys Ile Tyr Ala Asp Arg Leu Glu Gly Glu
 485 490 495
 Gly Val Ala Ser Gln Glu Asp Ala Thr Glu Met Val Asn Leu Tyr Arg
 500 505 510
 Asp Ala Leu Asp Ala Gly Glu Cys Val Val Pro Glu Trp Arg Pro Met
 515 520 525
 Ser Leu His Ser Phe Thr Trp Ser Pro Tyr Leu Asn His Glu Trp Asp
 530 535 540
 Glu Pro Tyr Pro Ala Gln Val Asp Met Lys Arg Leu Lys Glu Leu Ala
 545 550 555 560
 Leu Arg Ile Ser Gln Val Pro Glu Gln Ile Glu Val Gln Ser Arg Val
 565 570 575
 Ala Lys Ile Tyr Asn Asp Arg Lys Leu Met Ala Glu Gly Glu Lys Ala
 580 585 590
 Phe Asp Trp Gly Gly Ala Glu Asn Leu Ala Tyr Ala Thr Leu Val Asp
 595 600 605
 Glu Gly Ile Pro Val Arg Leu Ser Gly Glu Asp Ser Gly Arg Gly Thr
 610 615 620
 Phe Phe His Arg His Ala Val Val His Asn Gln Ala Asn Gly Ser Thr
 625 630 635 640
 Tyr Thr Pro Leu His His Ile His Asn Ser Gln Gly Glu Phe Lys Val
 645 650 655
 Trp Asp Ser Val Leu Ser Glu Glu Ala Val Leu Ala Phe Glu Tyr Gly
 660 665 670
 Tyr Ala Thr Ala Glu Pro Arg Val Leu Thr Ile Trp Glu Ala Gln Phe
 675 680 685
 Gly Asp Phe Ala Asn Gly Ala Gln Val Val Ile Asp Gln Phe Ile Ser
 690 695 700

Ser Gly Glu Gln Lys Trp Gly Arg Met Cys Gly Leu Val Met Leu Leu
 705 710 715 720
 Pro His Gly Tyr Glu Gly Gln Gly Pro Glu His Ser Ser Ala Arg Leu
 725 730 735
 Glu Arg Tyr Leu Gln Leu Cys Ala Glu Gln Asn Met Gln Val Cys Val
 740 745 750
 Pro Ser Thr Pro Ala Gln Val Tyr His Met Leu Arg Arg Gln Ala Leu
 755 760 765
 Arg Gly Met Arg Arg Pro Leu Val Val Met Ser Pro Lys Ser Leu Leu
 770 775 780
 Arg His Pro Leu Ala Ile Ser Ser Leu Asp Glu Leu Ala Asn Gly Ser
 785 790 795 800
 Phe Gln Pro Ala Ile Gly Glu Ile Asp Asp Leu Asp Pro Gln Gly Val
 805 810 815
 Lys Arg Val Val Leu Cys Ser Gly Lys Val Tyr Tyr Asp Leu Leu Glu
 820 825 830
 Gln Arg Arg Lys Asp Glu Lys Thr Asp Val Ala Ile Val Arg Ile Glu
 835 840 845
 Gln Leu Tyr Pro Phe Pro His Gln Ala Val Gln Glu Ala Leu Lys Ala
 850 855 860
 Tyr Ser His Val Gln Asp Phe Val Trp Cys Gln Glu Glu Pro Leu Asn
 865 870 875 880
 Gln Gly Ala Trp Tyr Cys Ser Gln His His Phe Arg Asp Val Val Pro
 885 890 895
 Phe Gly Ala Thr Leu Arg Tyr Ala Gly Arg Pro Ala Ser Ala Ser Pro
 900 905 910
 Ala Val Gly Tyr Met Ser Val His Gln Gln Gln Gln Asp Leu Val
 915 920 925
 Asn Asp Ala Leu Asn Val Asn
 930 935

<210> 4
 <211> 407
 <212> PRT
 <213> Enterobacter agglomerans

<400> 4
 Met Ser Ser Val Asp Ile Leu Val Pro Asp Leu Pro Glu Ser Val Ala
 1 5 10 15
 Asp Ala Thr Val Ala Thr Trp His Lys Lys Pro Gly Asp Ala Val Ser
 20 25 30
 Arg Asp Glu Val Ile Val Glu Ile Glu Thr Asp Lys Val Val Leu Glu
 35 40 45
 Val Pro Ala Ser Ala Asp Gly Val Leu Glu Ala Val Leu Glu Asp Glu
 50 55 60
 Gly Ala Thr Val Thr Ser Arg Gln Ile Leu Gly Arg Leu Lys Glu Gly
 65 70 75 80
 Asn Ser Ala Gly Lys Glu Ser Ser Ala Lys Ala Glu Ser Asn Asp Thr
 85 90 95
 Thr Pro Ala Gln Arg Gln Thr Ala Ser Leu Glu Glu Glu Ser Ser Asp
 100 105 110
 Ala Leu Ser Pro Ala Ile Arg Arg Leu Ile Ala Glu His Asn Leu Asp
 115 120 125
 Ala Ala Gln Ile Lys Gly Thr Gly Val Gly Gly Arg Leu Thr Arg Glu

130 135 140
 Asp Val Glu Lys His Leu Ala Asn Lys Pro Gln Ala Glu Lys Ala Ala
 145 150 155 160
 Ala Pro Ala Ala Gly Ala Ala Thr Ala Gln Gln Pro Val Ala Asn Arg
 165 170 175
 Ser Glu Lys Arg Val Pro Met Thr Arg Leu Arg Lys Arg Val Ala Glu
 180 185 190
 Arg Leu Leu Glu Ala Lys Asn Ser Thr Ala Met Leu Thr Thr Phe Asn
 195 200 205
 Glu Ile Asn Met Lys Pro Ile Met Asp Leu Arg Lys Gln Tyr Gly Asp
 210 215 220
 Ala Phe Glu Lys Arg His Gly Val Arg Leu Gly Phe Met Ser Phe Tyr
 225 230 235 240
 Ile Lys Ala Val Val Glu Ala Leu Lys Arg Tyr Pro Glu Val Asn Ala
 245 250 255
 Ser Ile Asp Gly Glu Asp Val Val Tyr His Asn Tyr Phe Asp Val Ser
 260 265 270
 Ile Ala Val Ser Thr Pro Arg Gly Leu Val Thr Pro Val Leu Arg Asp
 275 280 285
 Val Asp Ala Leu Ser Met Ala Asp Ile Glu Lys Lys Ile Lys Glu Leu
 290 295 300
 Ala Val Lys Gly Arg Asp Gly Lys Leu Thr Val Asp Asp Leu Thr Gly
 305 310 315 320
 Gly Asn Phe Thr Ile Thr Asn Gly Gly Val Phe Gly Ser Leu Met Ser
 325 330 335
 Thr Pro Ile Ile Asn Pro Pro Gln Ser Ala Ile Leu Gly Met His Ala
 340 345 350
 Ile Lys Asp Arg Pro Met Ala Val Asn Gly Gln Val Val Ile Leu Pro
 355 360 365
 Met Met Tyr Leu Ala Leu Ser Tyr Asp His Arg Leu Ile Asp Gly Arg
 370 375 380
 Glu Ser Val Gly Tyr Leu Val Ala Val Lys Glu Met Leu Glu Asp Pro
 385 390 395 400
 Ala Arg Leu Leu Leu Asp Val
 405

<210> 5
 <211> 40
 <212> PRT
 <213> Enterobacter agglomerans

<400> 5
 Met Asn Leu His Glu Tyr Gln Ala Lys Gln Leu Phe Ala Arg Tyr Gly
 1 5 10 15
 Met Pro Ala Pro Thr Gly Tyr Ala Cys Thr Thr Pro Arg Glu Ala Glu
 20 25 30
 Glu Ala Ala Ser Lys Ile Gly Ala
 35 40

<210> 6
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 6
gtcgacaata gccygaatct gttctggtcg 30

<210> 7
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 7
aagcttatcg acgctcccct cccacccgtt 30

Claims

1. A microorganism which can metabolize a carbon source at a specific pH in a liquid medium containing L-glutamic acid at a saturation concentration and the carbon source, and has ability to accumulate L-glutamic acid in an amount exceeding the amount corresponding to the saturation concentration in the liquid medium at the pH.
2. The microorganism according to claim 1, which can grow in the liquid medium.
3. The microorganism according to claim 1 or 2, wherein the pH is not more than 5.0.
4. The microorganism according to any one of claims 1-3, which has at least one of the following characteristics:
 - (a) the microorganism is enhanced in activity of an enzyme that catalyzes a reaction for biosynthesis of L-glutamic acid; and
 - (b) the microorganism is decreased in or deficient in activity of an enzyme that catalyzes a reaction branching from a biosynthetic pathway of L-glutamic acid and producing a compound other than L-glutamic acid.
5. The microorganism according to claim 4, wherein the enzyme that catalyzes the reaction for biosynthesis of L-glutamic acid is at least one selected from citrate synthase, phosphoenolpyruvate carboxylase and glutamate dehydrogenase.
6. The microorganism according to claim 4 or 5, wherein the enzyme that catalyzes the reaction branching from the biosynthetic pathway of L-glutamic acid and producing the compound other than L-glutamic acid is α -ketoglutarate dehydrogenase.
7. The microorganism according to any one of claims 1-6, wherein the microorganism belongs to the genus *Enterobacter*.
8. The microorganism according to claim 7, which is *Enterobacter agglomerans*.
9. The microorganism according to any of the claims 1 to 8, which contains the nucleotide sequence of SEQ ID No. 1.
10. A microorganism having the accession number FERM BP-6614.
11. A microorganism having the accession number FERM BP-6615.

12. A microorganism having the accession number FERM BP-7207.

13. The microorganism according to claim 8, which has a mutation that causes less extracellular secretion of a viscous material compared with a wild strain when cultured in a medium containing a saccharide.

5

14. A method for producing L-glutamic acid by fermentation, which comprises culturing a microorganism as defined in any one of claim 1-13 in a liquid medium of which pH is adjusted to a pH at which L-glutamic acid is precipitated, to produce and accumulate L-glutamic acid and precipitate L-glutamic acid in the medium.

10

15. A method for screening a microorganism suitable for producing L-glutamic acid by fermentation with precipitating L-glutamic acid in a liquid medium, which comprises inoculating a sample containing microorganisms into an acidic medium containing L-glutamic acid at a saturation concentration and a carbon source, and selecting a strain that can metabolize the carbon source.

15

16. The method according to claim 15 wherein a strain that can grow in the medium is selected as the strain that can metabolize the carbon source.

17. The method according to claim 15 or 16, wherein a pH of the medium is not more than 5.0.

20

25

30

35

40

45

50

55

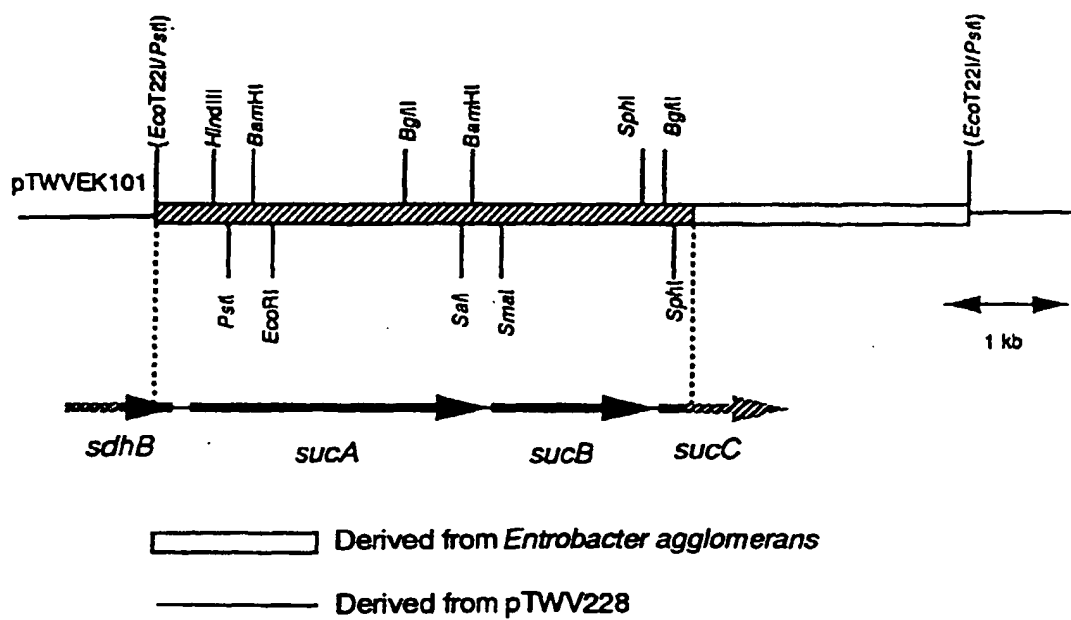


Fig. 1

[88.0% / 935 aa]

```

1'  MQNSAMKPYLDSSWLAGANQSYIEQLYEDFLTDPSVDVWRSWFQQLPGTGVKPEQFHS
   .....
1"  MQNSALKAMLDSSYLSGANQSWIEQLYEDFLTDPSVDANWRSTFQQLPGTGVKPDQFHS

61'  ATREYFRRLAKDASRYTSSVTPATNSKQVKVLQLINAFRFRGHQEANLOPLGLWKQORV
   .....
61"  QTREYFRRLAKDASRYSTISDPOTNVKQVKVLQLINAYRFRGHQHANLOPLGLWQQDKV

121'  ADLOPAFHDLTDAADFQESFMVGSFAIGKETMKLADLFDALKQTYCGSIGAEYMHINMTEE
   .....
121"  ADLOPSFHDLTEADFQETFMVGSFASGKETMKLGELLEALKQTYCGPIGAEYMHITSTEE

181'  KRWIQQRIESGASQTSFSGEEKKGFLKELTAAEGLEKYLGAKEFGAKRFSLEGGDALVPM
   .....
181"  KRWIQQRIESG--RATFNSEEKKRFLSELTAAEGLERYLGAKEFGAKRFSLEGGDALIPM

241'  LREMIRHAGKSGTREVVLMMAHRGRLNVLINVLGKKPQDLDEFSGKHKEHLGTGOVKYH
   .....
239"  LKEMIRHAGKSGTREVVLMMAHRGRLNVLNVLGKKPQDLDEFAGKHKEHLGTGOVKYH

301'  MGFSSDIETEGGLVHLALAFNPShLEIVSPVVMGsvRARLDRlaEPVSNKVLPItiHGDA
   .....
299"  MGFSSDFQTDGGLVHLALAFNPShLEIVSPVViGsvRARLDRlDEPSShKVLPItiHGDA

361'  AVIGQGVVQETLNMSQARGYEVGGTVRIVINNQGFTTShPKDARSTPYCTOiGKMVLAP
   .....
359"  AVTGQGVVQETLNMSKARGYEVGGTVRIVINNQGFTTShPLDARSTPYCTOiGKMVQAP

421'  IFHVNADPEAVAFVTRLALDyrNTfKRdVFIDLvCYRRHGhNEADePSATQPLMYQKiK
   .....
419"  IFHVNADPEAVAFVTRLALDFRNTfKRdVFIDLvSYRRHGhNEADePSATQPLMYQKiK

481'  KHPTPRKIYADRLLEGVAsQEDaTEMvNLYRDALDAGeCVvPEWRPMShSFTWSPYLN
   .....
479"  KHPTPRKIYADKLEQEKVATLEaTEMvNLYRDALDAGDcVvAEWRPMhShSFTWSPYLN

541'  HEWDEYPYQVDMKRLKELALRISQVPEQIEVQSRVAKIYNDRKLMAEGEKAFOWGGAEN
   .....
539"  HEWDEEYPNKVEMKRLQELAKRISTVPEAVEMQSRVAKIYGDRQAMAAGEKLFOWGGAEN

601'  LAYATLVDEGIPVRLSGEDSGRGTFFHRHAVVHNQANGSTYTPLHHIHNSQGEFKVWDSV
   .....
599"  LAYATLVDEGIPVRLSGEDSGRGTFFHRHAVIHNSNGSTYTPLQHINHNGQAFRVWDSV

661'  LSEEAVLAFeyGYATAePRVLTiWEAQFGDFANGAQVViDQFISSGEQKNGRMCLVMLL
   .....
659"  LSEEAVLAFeyGYATAePRTLtiWEAQFGDFANGAQVViDQFISSGEQKNGRMCLVMLL

721'  PHGYEGQGPEHSSARLERYLQLCAEQNMQVCVPSTPAQVYHMLRRQALRGMRPLVVMSP
   .....
719"  PHGYEGQGPEHSSARLERYLQLCAEQNMQVCVPSTPAQVYHMLRRQALRGMRPLVVMSP

781'  KSLLRHPLAISSLOELANGSFQPAIGEIDOLDPQGVKRVVLCsgKvYYDLLEQRKkDEKT
   .....
779"  KSLLRHPLAVSSLEELANGTFLPAIGEIDELDPKGVKRVVMCSgKvYYDLLEQRKkNNQH

841'  DVAIVRIEQLYPFPHQAVQEALKAYSHVQDFVWCQEELNQGAMyCSQHhFRDvVPFGAT
   .....
839"  DVAIVRIEQLYPFPHKAMQEVLLQFAHVKDFVWCQEELNQGAMyCSQHhFREVIpFGAS

901'  LRYAGRPASASPavGYMSVhQQQQQDLVNDALNVH
   .....
899"  LRYAGRPASASPavGYMSVhQKQQQDLVNDALNVE

```

Fig. 2

[88.2% / 407 aa]

```

1'  MSSVDILVPDLPESVADATVATMHHKXPGDAVSDEIVIEIETDKVLEVPASADGVLEAV
.....
1'  MSSVDILVPDLPESVADATVATMHHKXPGDAVVRDEVLEIETDKVLEVPASADGILDAV

61'  LEDEGATVTSRQILGRLKEGNSAGKESAKAESNOTTPAQRQTASLEES SOALSPAIRR
.....
61'  LEDEGTTVTSRQILGRLREGNSACKETSAKSEEKASTPAQRQQASLEEQHNDALSPAIRR

121'  LIAEHNLDAAQIKGTGVGGRLTREDVEKHLANKPQAEKAAAPAGAATAQQPVAMRSEKR
.....
121'  LIAEHNLDASAIXGTGVGGRLTREDVEKHLAKAPAKE--SAPAAAAPAAQPALAARSEKR

181'  VPMTRLRKRVAERLLEAKNSTAMLTTFNEIHHKPIHDLRKQYGDAFEKRGVRLGFMSFY
.....
179'  VPMTRLRKRVAERLLEAKNSTAMLTTFNEVHHKPIHDLRKQYGEAFEKRGHGRVRLGFMSFY

241'  IKAWVEALKRYPEVNASIDGEDVYHNYFDVSIIVSTPRGLVTPVLROVDALSHADIEKK
.....
239'  VKAWVEALKRYPEVNASIDGDDVYHNYFDVSMVSTPRGLVTPVLROVDLGMADIEKK

301'  IKELAVKGRDGKLTVDOLTGGNFTITNGGVFGSLMSTPIINPPQSAILGMHAIKDRPMAY
.....
299'  IKELAVKGRDGKLTVEOLTGGNFTITNGGVFGSLMSTPIINPPQSAILGMHAIKDRPMAY

361'  NGQVILPMMYLALSVDHRLIDGRESVGYLVAVKEHLEDPARLLLOV
.....
359'  NGQVEILPMMYLALSVDHRLIDGRESVGYLVAVKEHLEDPARLLLOV

```

Fig. 3

[95.1% / 41 aa]

```

1'  MNLHEYQAKQLFARYQMPAPTGYACTTPREAEAAASKIGAG
.....
1'  MNLHEYQAKQLFARYGLPAPVGYACTTPREAEAAASKIGAGPMVVKCQVHAGGRGKAGGV

```

Fig. 4

[97.4% / 39 aa]

```

1'  AFSVFRCHSIMNCVSVCPKGLNPTRAIGHIKSMLLQRSA
.....
181'  FLIDSRDTETDSRLDGLSDAFSVFRCHSIMNCVSVCPKGLNPTRAIGHIKSMLLQRNA

```

Fig. 5

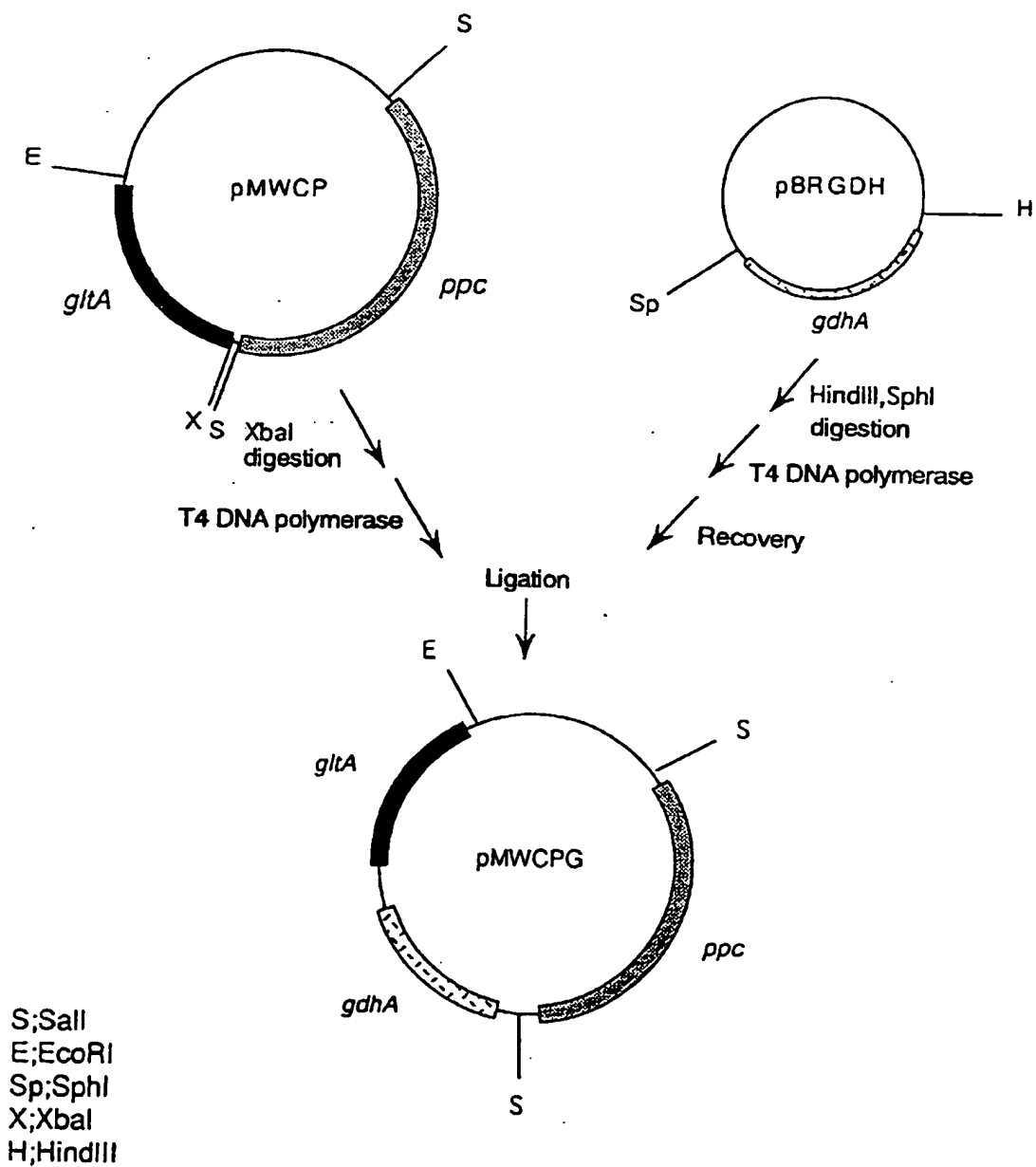


Fig. 6

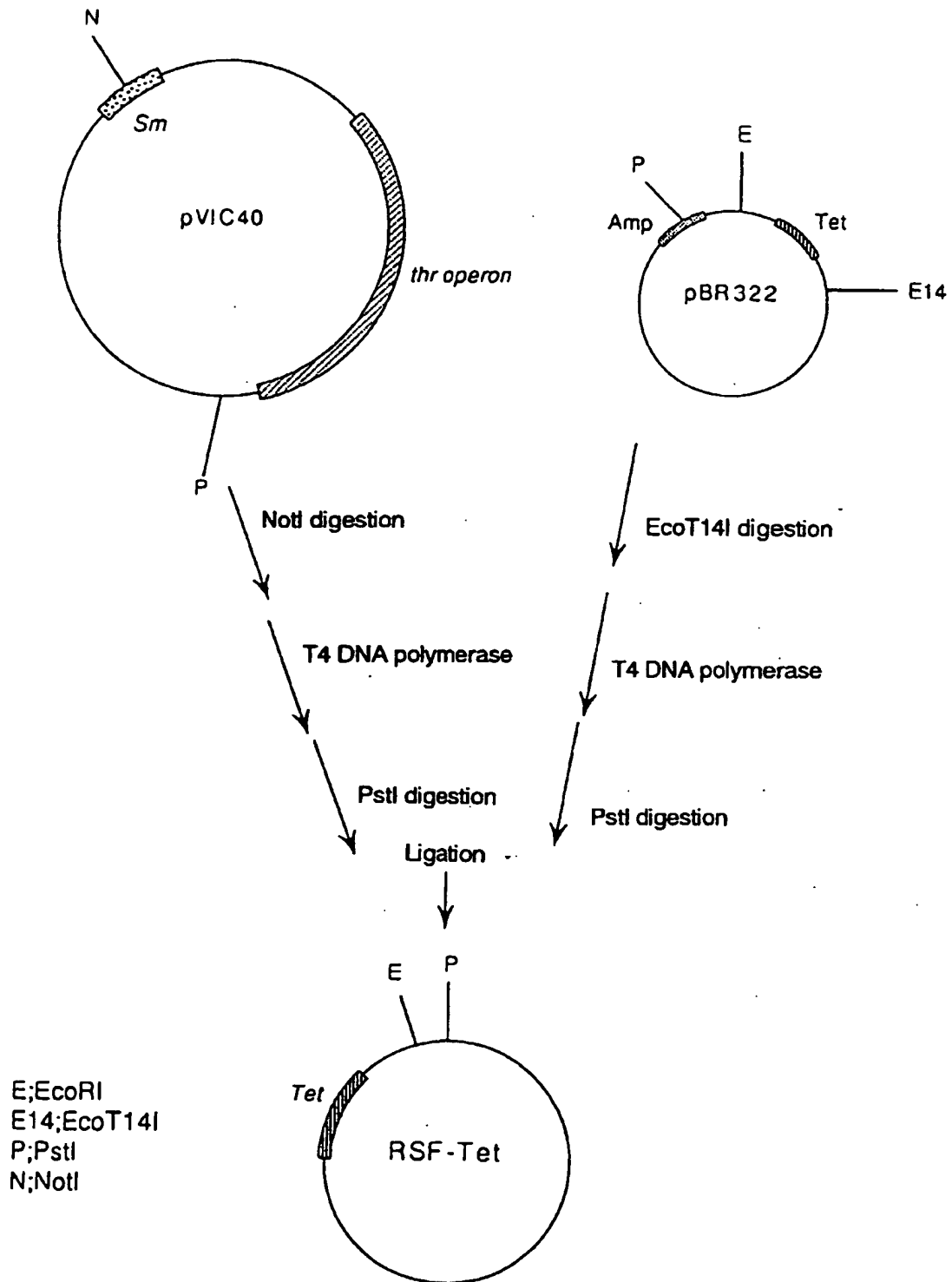


Fig. 7

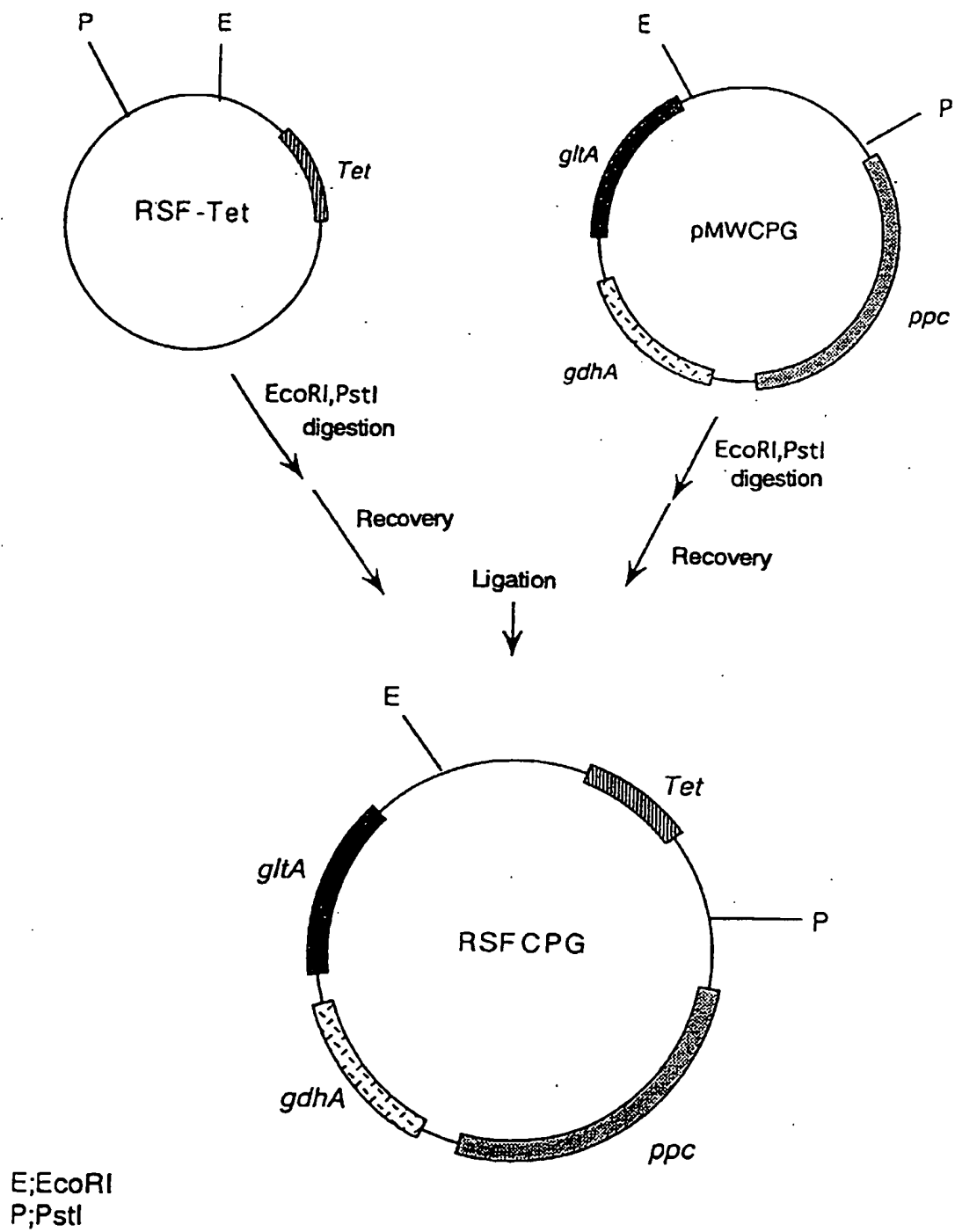


Fig. 8

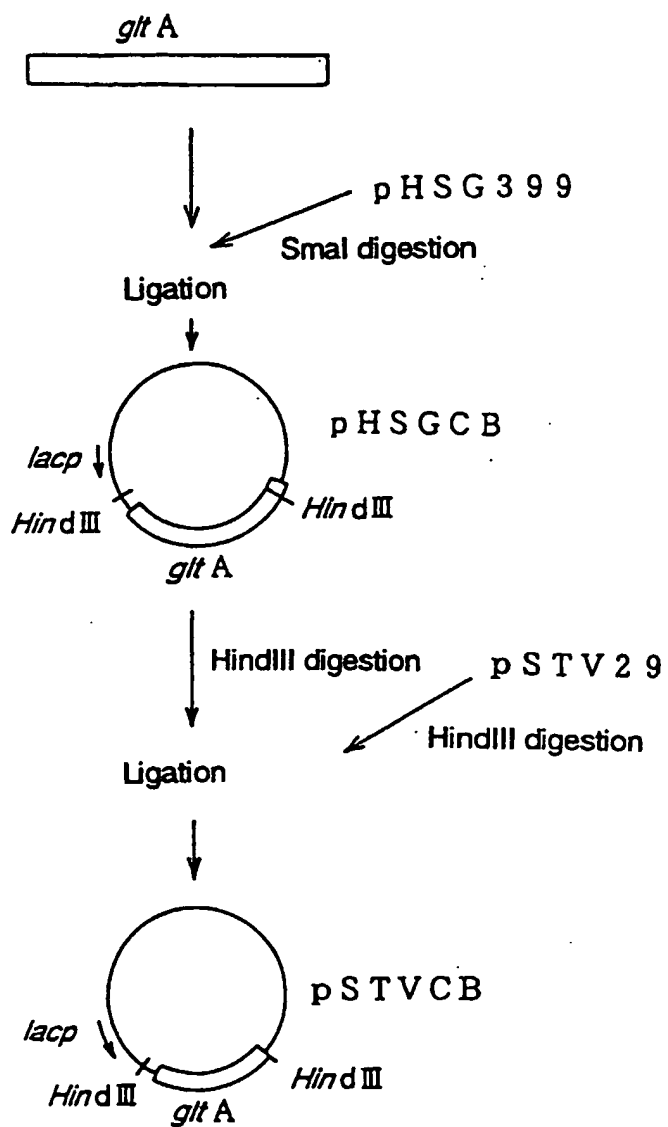


Fig. 9